

SEARCH REQUEST FORM

78/92

Requestor's Name: _____ Serial Number: _____

Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

STAFF USE ONLY

Date completed: 10/21/92
Searcher: Jan
Terminal time: _____
Elapsed time: 10
CPU time: +10
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site

_____ STIC
_____ ☒ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ ☒ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ ☒ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ Other

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2002, 07:46:28 ; Search time 27 Seconds
(without alignments)
1275.037 Million cell updates/sec

Title: US-09-823-307C-2
Perfect score: 1082
Sequence: 1 MKSGLMWFYFLCLRIKVLTFG.....YMFMRVAVNTAKKSRLTDVTL 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Tr: number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTRMBL_19: *
1: sp-archaea: *
2: sp-bacteria: *
3: sp-fungi: *
4: sp-human: *
5: sp-invertebrate: *
6: sp-mammal: *
7: sp-mhc: *
8: sp-organelle: *
9: sp-phage: *
10: sp-plant: *
11: sp-rodent: *
12: sp-virus: *
13: sp-vertebrate: *
14: sp-unclassified: *
15: sp-rvirus: *
16: sp-bacteriaph: *
17: sp-archaeap: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1082	100.0	199	4	Q9Y6W8	Q9Y6W8 homo sapien
2	737.5	68.2	200	11	Q9WVS0	Q9WVS0 mus musculu
3	734	67.8	200	11	Q9JL17	Q9JL17 mus musculu
4	701	64.8	200	11	Q9R1T7	Q9R1T7 rattus norv
5	696	64.3	216	11	Q9WVR9	Q9WVR9 rattus norv
6	146.5	13.5	221	6	Q9JLV4	Q9JLV4 marmota mon
7	145.5	13.4	221	6	Q9N2I4	Q9N2I4 felis silve
8	145.5	13.4	221	6	002757	002757 felis silve
9	145	13.4	219	6	Q97630	Q97630 ovis aries
10	140.5	13.0	221	6	Q9GKP3	Q9GKP3 canis famil
11	140.5	13.0	221	6	Q9N0N8	Q9N0N8 canis famil
12	139.5	12.9	173	6	Q28289	Q28289 canis famil
13	136.5	12.6	220	6	Q9BDM8	Q9BDM8 macaca neme
14	135.5	12.5	220	6	Q9BDN5	Q9BDN5 cercocobus
15	130.5	12.1	220	6	Q9BDM6	Q9BDM6 macaca mula
16	125.5	11.6	220	6	Q9BDN8	Q9BDN8 papio anubi

17	115.5	10.7	220	6	Q9BDN2	Q9BDN2 callithrix
18	103.5	9.6	988	5	Q17710	Q17710 caenorhabdi
19	91.5	8.5	485	5	Q20139	Q20139 caenorhabdi
20	87	8.0	223	6	Q9BDP1	Q9BDP1 aotus trivi
21	84.5	7.8	209	4	Q9NYK4	Q9NYK4 homo sapien
22	84.5	7.8	223	11	Q9QZ27	Q9QZ27 mus musculu
23	84	7.8	223	4	Q96P43	Q96P43 homo sapien
24	84	7.8	285	17	Q28747	Q28747 archaeglob
25	84	7.8	419	13	Q9IA91	Q9IA91 morone saxa
26	83.5	7.7	223	11	Q9JLV3	Q9JLV3 marmota mon
27	83	7.7	1239	10	Q9FHM1	Q9FHM1 arabidopsis
28	82.5	7.6	223	11	Q62859	Q62859 rattus norv
29	82	7.6	223	6	Q9BDC4	Q9BDC4 macaca mula
30	82	7.6	223	6	Q9BDN7	Q9BDN7 papio anubi
31	81	7.5	276	12	Q98822	Q98822 human adeno
32	81	7.5	276	12	Q64861	Q64861 human adeno
33	81	7.5	680	11	Q55001	Q55001 mus musculu
34	80.5	7.4	247	16	Q99RX6	Q99RX6 staphylococ
35	80.5	7.4	635	11	Q55002	Q55002 mus musculu
36	80.5	7.4	663	11	Q70434	Q70434 mus musculu
37	79.5	7.3	269	4	Q95297	Q95297 homo sapien
38	79	7.3	370	4	Q9BZM8	Q9BZM8 homo sapien
39	78.5	7.3	310	11	Q9EQ87	Q9EQ87 mus musculu
40	78	7.2	231	5	Q45668	Q45668 caenorhabdi
41	77.5	7.2	311	11	Q9EQ86	Q9EQ86 mus musculu
42	77	7.1	323	6	Q9BDM2	Q9BDM2 cercopithec
43	77	7.1	338	5	Q22576	Q22576 caenorhabdi
44	77	7.1	539	12	P88842	P88842 avian infec
45	77	7.1	619	10	Q9XG61	Q9XG61 sorghum bic

ALIGNMENTS

RESULT 1
Q9Y6W8 ID Q9Y6W8 PRELIMINARY; PRT; 199 AA.
AC Q9Y6W8;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE AILIM
DE PRECURSOR (INDUCIBLE T-CELL CO-STIMULATOR PRECURSOR) (INDUCIBLE
DE COSTIMULATOR PRECURSOR).
GN ICOS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Tezuka K., Tamatani T.;
RT "Cell surface molecule mediating cell adhesion and signal
transmission.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99127892; PubMed=9930702;
RA Hultlof A., Dittrich A.M., Beier K.C., Eljaschewitsch B., Kraft R.,
RA Anagnostopoulos I., Krocze R.A.;
RT "ICOS is an inducible T-cell co-stimulator structurally and
functionally related to CD28.";
RL Nature 397:263-266(1999).
[3]
RP SEQUENCE FROM N.A.
RA Beier K.C., Hultlof A., Dittrich A.M., Heuck C., Mages H.W.,
RA Buechner K., Henn V., Rauch A., Krocze R.A.;
RT "Detailed analysis of human ICOS and its ligand.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;

```

RX MEDLINE-20243570;
RA Aicher A., Hayden-Ledbetter M., Brady W.A., Pezzutto A., Richter G.,
RA Magaletti D., Buckwalter S., Ledbetter J.A., Clark E.A.;
RT "Characterization of human inducible costimulator ligand expression
RT and function.";
RL J. Immunol. 164:4689-4696(2000).
DR EMBL; AB023135; BAA82129.1; -
DR EMBL; AJ277832; CAC06612.1; -
DR EMBL; AF218312; AAF71301.1; -
KW Signal.
FT SIGNAL.
SQ SEQUENCE 1 20 POTENTIAL.
Query Match 100.0%; Score 1082; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 2.8e-109;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSGMYEFLFCLRIKVLTEINGSANYEMFIHNGVQILCKYPDIVOQFKMQLKGQ 60
1 MKSGMYEFLFCLRIKVLTEINGSANYEMFIHNGVQILCKYPDIVOQFKMQLKGQ 60

LY 61 ILCDLTKTSGSNTVSISLKFCHSOLSNNVSFPLYNLDSHANYFCNLSIFDPPPK 120
61 ILCDLTKTSGSNTVSISLKFCHSOLSNNVSFPLYNLDSHANYFCNLSIFDPPPK 120

DB 121 VTLLGYLHIYESQLCCQKFWLPICGAFVWCILGCLICWLTKRKKSSSVHDPNGEY 180
121 VTLLGYLHIYESQLCCQKFWLPICGAFVWCILGCLICWLTKRKKSSSVHDPNGEY 180

QY 121 VTLLGYLHIYESQLCCQKFWLPICGAFVWCILGCLICWLTKRKKSSSVHDPNGEY 180
121 VTLLGYLHIYESQLCCQKFWLPICGAFVWCILGCLICWLTKRKKSSSVHDPNGEY 180

DB 121 VTLLGYLHIYESQLCCQKFWLPICGAFVWCILGCLICWLTKRKKSSSVHDPNGEY 180
121 VTLLGYLHIYESQLCCQKFWLPICGAFVWCILGCLICWLTKRKKSSSVHDPNGEY 180

QY 181 MEMRAVNTAKKSRLTDVTL 199
181 MEMRAVNTAKKSRLTDVTL 199

DB 181 MEMRAVNTAKKSRLTDVTL 199
181 MEMRAVNTAKKSRLTDVTL 199

RESULT 2
O9WVS0 PRELIMINARY; PRT; 200 AA.
ID O9WVS0;
AC O9WVS0;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE AILIM
DE PRECURSOR (CCLP PRECURSOR) (SURFACE PROTEIN).
OS CCLP OR ICOS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
TISSUE=SPLEEN;
Tezuka K., Tamatani T.;
"Cell surface molecule mediating cell adhesion and signal
transmission.";
Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE=SPLEEN;
Wu D., Giannoni M.A., Kiesecker C.L., Faas S.J., Mickle A.P.,
Matis L.A., Rother R.P.;
"CCLP, A novel molecule that regulates T cell activation.";
Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE=SPLEEN;
MEDLINE-20225659; PubMed-10760791;
Mages H.W., Hutloff A., Heuck C., Buchner K., Himmelbauer H.,
Oliveri F., Krocze R.A.;
"Molecular cloning and characterization of murine ICOS and
identification of B7h as ICOS ligand.";
Eur. J. Immunol. 30:1040-1047(2000).
DR EMBL; AB023132; BAA82126.1; -
DR EMBL; AF257230; AAF70099.1; -

```

```

DR EMBL; AJ250559; CAB71153.1; -.
DR MGD; MG1:1858745; ICOS.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 1 20 POTENTIAL.
Query Match 68.2%; Score 737.5; DB 11; Length 200;
Best Local Similarity 69.3%; Pred. No. 6e-72;
Matches 138; Conservative 20; Mismatches 40; Indels 1; Gaps 1;
QY 1 MKSGLMYFELFLCRIRKVLGTGEINGSANYEMFIHNGGVQILCKYPDVIQOEFKMQLKGQ 60
DB 1 MKPFCVHFVEFCFLIRLTGTGEINGSADHRMFSFHNGGVQISCKYPEVTVOOLKMLFRERE 60
QY 61 ILCDLTKTKGSGNTVSISKSLEKCHSOLSNNNSVSFFLYNLDSHANYEFCNLSIFDPPPFK 120
DB 61 VLCELTKTGSGNAVSIKNPMCLYLHSNNNSVSFFLNPNDDSSOGSYIFCSLSIFDPPPFQ 120
QY 121 V-TLTGGYLHIYESQLCCOLKEWLPICCAAFVVVCILGCILCWLTKKKYSSSVHPDNGE 179
DB 121 ERNMSGYLHIYESQLCCOLKEWLPICCAAFVVLLFGCILIMESKKKYGSVDHPNSE 180
QY 180 YMFRAVNTAKKSRLTDVT 198
DB 181 YMFAAVNTNKSKSLAGVT 199
RESULT 3
Q9JL17 PRELIMINARY; PRT; 200 AA.
AC Q9JL17;
AT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
CD CD28-RELATED PROTEIN 1 (INDUCIBLE COSTIMULATORY PROTEIN)
DE (FRAGMENT).
GN ICOS.
NM Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP TISSUE=INTRESTINAL INTRA-EPIITHELIUM;
RC YOSHINAGA S.K., WHORISKKEY J.S., KHARE S.D., SARMENTO U., GUO J.,
RA HORAN T., SHIH G., ZHANG M., COCCIA M.A., KOHNO T., TAFURI-BLADT A.,
RA CAMPBELL P., CHANG D., CHIU L., DAI T., DUNCAN G., ELLIOTT G.S.,
RA HUI A., MCCABE S.M., SCULLY S., SHAKLEE C.L., VAN G., MAK T.W.,
RA SENALDI G.;
RT "T-cell co-stimulation through B7RP-1 and ICOS.";
RL Nature 0:0-0(2000).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/OLA;
RA McAdam A.J., Greenwald R.J., Levin M.A., Chernova T., Malenkovich N.,
RA Ling V., Freeman G.J., Sharpe A.H.;
RT "The inducible costimulatory (ICOS) molecule is critical for CD40-
RT mediated antibody class switching."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF216748; AAF45150.1; -.
DR EMBL; AF327185; AAG48732.1; -.
DR EMBL; AF327184; AAG48732.1; JOINED.
FT NON_TER 200
SQ SEQUENCE 200 AA; 22709 MW; 87D97FD0DC44ADC47 CRC64;
Query Match 67.8%; Score 734; DB 11; Length 200;
Best Local Similarity 70.4%; Pred. No. 1.4e-71;
Matches 138; Conservative 19; Mismatches 35; Indels 4; Gaps 2;
QY 7 YF---FLFCLRIRKVLGTGEINGSANYEMFIHNGGVQILCKYPDVIQOEFKMQLKGQILC 63
DB 4 YFCRVFVFECFLIRLTGTGEINGSADHRMFSFHNGGVQISCKYPEVTVOOLKMLFREREVLTC 63

```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2002, 07:46:28 : Search time 14 Seconds
(without alignments)
347.192 Million cell updates/sec

Title: US-09-823-307C-2
Perfect score: 1082
Sequence: 1 MKSGLMYFFLECLRIRKVLTG.....YMFMRVAVNTAKKSRLTDVTL 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	163	15.1	218	3 US-08-228-208A-20	Sequence 20, Appl
2	146.5	13.5	225	1 US-08-505-058-4	Sequence 4, Appl
3	146.5	13.5	225	2 US-08-459-818-24	Sequence 24, Appl
4	146.5	13.5	225	2 US-08-889-666-24	Sequence 24, Appl
5	146.5	13.5	225	2 US-08-465-078-24	Sequence 24, Appl
6	146.5	13.5	225	2 US-08-725-776-24	Sequence 24, Appl
7	146.5	13.5	225	2 US-08-488-062-24	Sequence 24, Appl
8	140	12.9	218	3 US-08-228-208A-19	Sequence 19, Appl
9	134.5	12.4	220	3 US-08-228-208A-21	Sequence 21, Appl
10	134	12.4	225	1 US-08-505-058-3	Sequence 3, Appl
11	134	12.4	225	2 US-08-459-818-23	Sequence 23, Appl
12	134	12.4	225	2 US-08-889-666-23	Sequence 23, Appl
13	134	12.4	225	2 US-08-465-078-23	Sequence 23, Appl
14	134	12.4	225	2 US-08-725-776-23	Sequence 23, Appl
15	134	12.4	225	2 US-08-488-062-23	Sequence 23, Appl
16	126	11.6	223	1 US-08-505-058-5	Sequence 5, Appl
17	126	11.6	223	2 US-08-459-818-25	Sequence 25, Appl
18	126	11.6	223	2 US-08-889-666-25	Sequence 25, Appl
19	126	11.6	223	2 US-08-465-078-25	Sequence 25, Appl
20	126	11.6	223	2 US-08-725-776-25	Sequence 25, Appl
21	126	11.6	223	2 US-08-488-062-25	Sequence 25, Appl
22	120.5	11.1	367	3 US-08-630-172-19	Sequence 19, Appl
23	120.5	11.1	367	4 US-09-375-419-19	Sequence 19, Appl
24	119.5	11.0	134	4 US-08-630-172-3	Sequence 3, Appl
25	119.5	11.0	134	4 US-09-375-419-3	Sequence 3, Appl
26	110.5	10.2	110	4 US-09-460-384-33	Sequence 33, Appl
27	93	8.6	221	3 US-08-228-208A-22	Sequence 22, Appl

28	89.5	8.3	117	2 US-08-529-878B-39	Sequence 39, Appl
29	87	8.0	330	2 US-08-332-562A-81	Sequence 81, Appl
30	87	8.0	330	2 US-08-332-562A-134	Sequence 134, Appl
31	86.5	8.0	209	4 US-09-430-503-20	Sequence 20, Appl
32	84.5	7.8	209	4 US-09-430-503-18	Sequence 18, Appl
33	84.5	7.8	209	4 US-09-430-503-24	Sequence 24, Appl
34	84	7.8	223	3 US-08-228-208A-17	Sequence 17, Appl
35	84	7.8	283	2 US-08-332-562A-136	Sequence 136, Appl
36	82.5	7.6	209	4 US-09-430-503-22	Sequence 22, Appl
37	81.5	7.5	187	1 US-08-067-684-14	Sequence 14, Appl
38	81.5	7.5	187	1 US-08-008-898-14	Sequence 14, Appl
39	81.5	7.5	187	2 US-08-459-818-14	Sequence 14, Appl
40	81.5	7.5	187	2 US-08-889-666-14	Sequence 14, Appl
41	81.5	7.5	187	2 US-08-465-078-14	Sequence 14, Appl
42	81.5	7.5	187	2 US-08-725-776-14	Sequence 14, Appl
43	81.5	7.5	187	2 US-08-488-062-14	Sequence 14, Appl
44	81.5	7.5	187	3 US-08-228-208A-14	Sequence 14, Appl
45	81.5	7.5	187	5 PCT-US95-06726-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-228-208A-20
Sequence 20, Application US/08228208A
Patent No. 6090914
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Wallace, Philip M.
TITLE OF INVENTION: CTLA4/CD28ig HYBRID FUSION
TITLE OF INVENTION: PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228, 208A
FILING DATE: 15-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/008, 898
FILING DATE: 22-JAN-1993
APPLICATION NUMBER: 07/723, 617
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-30US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310 445-1140
TELEFAX: 310 445-9031
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-228-208A-20

Query Match 15.1%; Score 163; DB 3; Length 218;
Best Local Similarity 26.5%; Pred. No. 3e-11; Mismatches 65; Indels 18; Gaps 7;
Matches 41; Conservative 31; Mismatches 65; Indels 18; Gaps 7;
OY 30 MFIHNGVQILCKYPD--IVQOFKMLKGGQILCDLTKT-KSGNTVSIKSLK-----F 82
DB 29 LLYVDNNEVSLSCRYSNLLKKEFRASLYKG--VNSDVEVCVGNNGFTYQOPFRPNVGFN 86
OY 83 CHSOLSNNSVSFFLYNLDSHANYFFCNLSIFDPPE--KVTLTGGLHYESQLC---C 137
DB 87 CDGNFNDNETVTFRLMNLVDVNHDTDYFCKIEVMYPPPYLDNEKSNGTIIHIKEKHLCHAQT 146
OY 138 QLKFWLPICGAFFVVC--ILGCILIC--WLTKKK 168
DB 147 SPKLFWPLVVAVGVLGCLLYTVTLCTIWTNSRR 181
RESULT 2
Sequence 4, Application US/08505058
Patent No. 5773253
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Peach, Robert
TITLE OF INVENTION: CTLA4 Mutant Molecules and Uses Thereof
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,058
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/228,208
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.30US11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-505-058-4
Query Match 13.5%; Score 146.5; DB 1; Length 225;
Best Local Similarity 26.2%; Pred. No. 2.7e-09;
Matches 42; Conservative 31; Mismatches 64; Indels 23; Gaps 9;
OY 30 MFIHNGVQIL-CKYPD--IVQOFKMLKGGQILCDLTKT-KSGNTVSIKSLK----- 81
DB 30 LLYVDNNEVXSLSCRYSNLLAKEFRASLYKG--VNSDVXEVCGVGNNGFTYQOPFRPNVG 87
OY 82 -FCHSOLSNNSVSFFLYNLDSHANYFCNLSIFDPPE--KVTLTGGLHYESQLC-- 136
DB 82 XXXQTSPLKFWPLVVAVGVLGCLLYTVTLCTIWTNSRR 187

DB 88 FNCDFNFDNETVTFRLMNLVDVNHDTDYFCKIEVMYPPPYLDNEKSNGTIIHIKEKHLCHA 147
OY 137 ----COLKFWLPICGAFFVVC--ILGCILIC--WLTKKK 168
DB 148 XXXQTSPLKFWPLVVAVGVLGCLLYTVTLCTIWTNSRR 187
RESULT 3
US-08-459-818-24
Sequence 24, Application US/08459818
Patent No. 5851795
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,818
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.35US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-818-24
Query Match 13.5%; Score 146.5; DB 2; Length 225;
Best Local Similarity 26.2%; Pred. No. 2.7e-09;
Matches 42; Conservative 31; Mismatches 64; Indels 23; Gaps 9;
OY 30 MFIHNGVQIL-CKYPD--IVQOFKMLKGGQILCDLTKT-KSGNTVSIKSLK----- 81
DB 30 LLYVDNNEVXSLSCRYSNLLAKEFRASLYKG--VNSDVXEVCGVGNNGFTYQOPFRPNVG 87
OY 82 -FCHSOLSNNSVSFFLYNLDSHANYFCNLSIFDPPE--KVTLTGGLHYESQLC-- 136
DB 88 FNCDFNFDNETVTFRLMNLVDVNHDTDYFCKIEVMYPPPYLDNEKSNGTIIHIKEKHLCHA 147
OY 137 ----COLKFWLPICGAFFVVC--ILGCILIC--WLTKKK 168
DB 148 XXXQTSPLKFWPLVVAVGVLGCLLYTVTLCTIWTNSRR 187
RESULT 4
US-08-889-666-24
Sequence 24, Application US/08889666
Patent No. 5885379
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.

```

; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 1150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,666
; FILING DATE: 08-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEO ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-889-666-24

```

	Query Match	Best Local Similarity	Matches	Score	Pred.	No.	DB	Length	Gaps
QY	30 MFIFHNGGVQIL-CKYPD--IVQDFKMOQLLKGQIICDLTKT-KGSGNTVSIKSLK----	13.5%;	42;	146.5;	26.2%;	31;	2;	225;	23;
D-	30 LLYVDNNEVXSLSCRSYNLAKERRASLYKG--VNSDVXEVCVGNGFTYQPFRPNVG	Conservative	42;	31;	Mismatches	64;	Indels	23;	Gaps
QY	82 -FCHSOLSNSSVSFFLYNLDSHANYFCNLSIFDPPF--KVTLTGCLHIYESQLC--	13.5%;	42;	146.5;	26.2%;	31;	2;	225;	23;
Db	88 FNCDGNFNDETFTFRLWNLVDVHTDIYFCKIEVMYPPRYLDNEKSNGTIHIKEKHLCHA	Conservative	42;	31;	Mismatches	64;	Indels	23;	Gaps
QY	137 ----COLKFWLPIGCAAFVVVC--ILGCILIC-WLTKKK	13.5%;	42;	146.5;	26.2%;	31;	2;	225;	23;
Db	148 XXXQTSPLKFLWPLVVAVAGVLICYGLTYVTLCIIWTNSRR	Conservative	42;	31;	Mismatches	64;	Indels	23;	Gaps

RESULT 5
US-08-465-078-24
Sequence 24, Application US/08465078
Patent No. 5885796
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould

```

1 STREET: 11150 Santa Monica Blvd., Suite 400
2 CITY: Los Angeles
3 STATE: California
4 COUNTRY: USA
5 ZIP: 90025
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: PatentIn Release #1.0, Version #1.30
12
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/465,078
15 FILING DATE: 05-JUN-1995
16 CLASSIFICATION: 435
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 08/375390
19 FILING DATE: 18-JAN-1995
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Adriano, Sarah B.
22 REGISTRATION NUMBER: 34,470
23 REFERENCE/DOCKET NUMBER: 30436-35US01
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: 310-445-1140
26 TELEFAX: 310-445-9031
27 INFORMATION FOR SEQ ID NO: 24:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 225 amino acids
30 TYPE: amino acid
31 STRANDEDNESS:
32 TOPOLOGY: linear
33 MOLECULE TYPE: protein
34
35 US-08-465-078-24
36
37 Query Match 13.5%; Score 146.5; DB 2; Length 225;
38 Best Local Similarity 26.2%; Pred. No. 2.7e-09;
39 Matches 42; Conservative 31; Mismatches 64; Indels 23; Gaps 9;
40
41 QY 30 MFIHNGVGVOIL-CKYPD--IVQEFKMLKGGQILDLTKT-KSGNTVSIKSLK---- 81
42 : : : | | | | : : : : : : : : : : : : : : : : : : : : : :
43 Db 30 LVIYDNNVXSLSCRYSLNLAKFRASLYKG--VNSDVXEVYCVGNNGFTYQOPFRPNVG 87
44
45 QY 82 -FCHSOLSNNSVSFFLYNLNLDHSNANYFCNLISFDPPF--KVTLLTGGLHIYESQLC-- 136
46 : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
47 Db 88 FNC DGNEDNETVTFRLMNDLVNHTDIYFCKIEVMYPPRYLDNEKSNGTIIHIKEKHLCHA 147
48
49 QY 137 ----CQLKFWLPIGCAAFVVC--ILGCILIC--WLTKKK 168
50 : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
51 Db 148 XXXQTSPLKFLFWLVVAVGLLCYGLLYTVTLCIWTSNR 187
52
53 RESULT 6
54 US-08-725-776-24
55 Sequence 24, Application US/08725776
56 Patent No. 5968510
57
58 GENERAL INFORMATION:
59 APPLICANT: Linsley, Peter S.
60 APPLICANT: Ledbetter, Jeffrey A.
61 APPLICANT: Damle, Nitin K.
62 APPLICANT: Brady, William
63 APPLICANT: Kienner, Peter A.
64 TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
65 NUMBER OF SEQUENCES: 26
66 CORRESPONDENCE ADDRESS:
67 ADDRESSEE: Merchant & Gould
68 STREET: 11150 Santa Monica Blvd., Suite 400
69 CITY: Los Angeles
70 STATE: California
71 COUNTRY: USA
72 ZIP: 90025
73
74 COMPUTER READABLE FORM:
75 MEDIUM TYPE: Floppy disk
76 COMPUTER: IBM PC compatible
77 OPERATING SYSTEM: PC-DOS/MS-DOS

```



```

SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,776
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-725-776-24

Query Match      13.5%; Score 146.5; DB 2; Length 225;
Best Local Similarity 26.2%; Pred. No. 2.7e-09;
Matches 42; Conservative 31; Mismatches 64; Indels 23; Gaps 9;

QY   30 MEIFHNGVQIL-CKYPD--IVQQFKMQLKGGQILCDLTKT-KGSGNTVSISLSK---- 81
    : : | | | | | : : | | | | : : | | | : : | | | : : | | | : : | | |
DB   30 LLYVDNNEVXSLSCRSYNMLAKEFRASLYKG--VNSDVXEVCVGNGNFTYQPQFRPNVG 87
QY   82 -FCHSOLSNNSVSFFFLYNDHSANYFCNLISFDPPPE--KVTLTGGLHYESQLC-- 136
    | : | | | | | | : : | | | : : | | | : : | | | : : | | | : : | | |
DB   88 FNCGDGFNETVTFRMLMDLVNHTDIYFCKIEVMYPPLDNEKSNGTIHIKEKHLCCHA 147
QY   137 ----COLKFWLPICGAFFVVC--ILGCILIC--WLTKKK 168
    | : | | | | | : : | | | : : | | | : : | | | : : | | | : : | | |
DB   148 XXXQTSPKLFWPLVVAVAGVLLCYGLLYTVTLCTIWTNSRR 187

RESULT 7
US-08-488-062-24
Sequence 24, Application US/08488062
Patent No. 5977318
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,062
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:

```

```

: NAME: Adriano, Sarah B.
: REGISTRATION NUMBER: 34,470
: REFERENCE/DOCKET NUMBER: 30436-35US01
: TELECOMMUNICATION INFORMATION:
:   TELEPHONE: 310-445-1140
:   TELEFAX: 310-445-9031
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 225 amino acids
:   TYPE: amino acid
:   STRANDEDNESS:
:   TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-488-062-24

Query Match      13.5%; Score 146.5; DB 2; Length 225;
Best Local Similarity 26.2%; Pred. No. 2.7e-09;
Matches 42; Conservative 31; Mismatches 64; Indels 23; Gaps 9;

QY 30 MEIFHNGVQIL-CKYPD--IVQOFKQLKGGQILCDLTKT-KSGNTVSISLKL---- 81
: ::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 30 LLVYDNEVXSLSCRYSYNLLAKEFRASLYKG--VNSDYXECVGNNGFTYQOFRPNVG 87
QY 82 -FCHSOLSNNSVSFELYNLDHSHANYFCNLSTFDPPPF--KVTLTGGYLHIYESQLC-- 136
: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 88 FNCDDGNFEDNETVTFRLNLDVNHDTIDYFCKIEVMYPPPYLDNEKSNGTIIHIKEKHLCHA 147
QY 137 ----COLKFWLPICGAFVVC--ILGCILIC--WLFKKR 168
: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 148 XXXQTSPLFWPLVYVAGVLLCYGLLYTTLCTIWTNSRR 187

RESULT 8
US-08-228-208A-19
: Sequence 19, Application US/08228208A
: Patent No. 6090914
: GENERAL INFORMATION:
:   APPLICANT: Linsley, Peter S.
:   APPLICANT: Ledbetter, Jeffrey A.
:   APPLICANT: Dample, Milton K.
:   APPLICANT: Brady, William
:   APPLICANT: Wallace, Philip M.
:   TITLE OF INVENTION: CTLA4/CD28I9 HYBRID FUSION
:   TITLE OF INVENTION: PROTEINS AND USES THEREOF
:   NUMBER OF SEQUENCES: 22
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: Merchant & Gould
:     STREET: 11150 Santa Monica Boulevard, Suite 400
:     CITY: Los Angeles
:     STATE: CA
:     COUNTRY: USA
:     ZIP: 90025
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Diskette
:   COMPUTER: IBM Compatible
:   OPERATING SYSTEM: DOS
:   SOFTWARE: FASTSEQ Version 2.0
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/08/228,208A
:   FILING DATE: 15-APR-1994
:   CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: 08/008,898
:   FILING DATE: 22-JAN-1993
:   APPLICATION NUMBER: 07/723,617
:   FILING DATE: 27-JUN-1991
: ATTORNEY/AGENT INFORMATION:
:   NAME: Adriano, Sarah B
:   REGISTRATION NUMBER: 34,470
:   REFERENCE/DOCKET NUMBER: 30436-30US01
:   TELECOMMUNICATION INFORMATION:
:     TELEPHONE: 310 445-1140
:     TELEFAX: 310 445-9031

```

```
TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-228-208A-19

Query Match          12.9%; Score 140; DB 3; Length 218;
Best Local Similarity 25.7%; Pred. No. 1.5e-08;
Matches 39; Conservative 24; Mismatches 61; Indels 28; Gaps 7;

QY 38 VQILCKYPD--IVQQFMQLKGGQILCDLTKTSGSNTVSIKSLK-----CHSGLSNM 90
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 37 VSLSCRYSYNLAKREFRASLYKG--VNSDVEVCVGNNGFTYQPFQFRSNAEFNCDGDFDNE 94
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 91 SVSEFLYNLDHSHANYFCNLISFDPPPF--KVTLTGGLHIYESQLC---COLKFWLP 144
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 95 TVTFRLWNLHVNHFTDIYFCKIEFMPYPPLDNEKSNGTIIHVKHKLCHTQSSPKLFW-- 152
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 145 IGCAAFVVCILGC-----ILICWLTKKK 168
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 153 --ALYVYAGVLEFCYGLLVTVALCVLTWNSRR 181
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 9
US-08-228-208A-21
; Sequence 21, Application US/08228208A
; Patent No. 6090914
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Wallace, Phillip M.
; TITLE OF INVENTION: CTLA4/CD28ig HYBRID FUSION
; TITLE OF INVENTION: PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,208A
; FILING DATE: 15-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/008,898
; FILING DATE: 22-JAN-1993
; APPLICATION NUMBER: 07/723,617
; FILING DATE: 27-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-30US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310 445-1140
; TELEFAX: 310 445-9031
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: amino acid
```

```
STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-228-208A-21

Query Match          12.4%; Score 134.5; DB 3; Length 220;
Best Local Similarity 25.4%; Pred. No. 6.8e-08;
Matches 44; Conservative 30; Mismatches 74; Indels 25; Gaps 7;

QY 30 MEIFHNGVQILCKYPD--IVQQFMQLKGGQILCDLTKTSGSN---TVSIKSLKFC 84
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 28 MLVAYDNAYNLSCRYSYNLFSREFRASLHKGLDSAIVECVYGNYSQQLQVYKSTGFNCD 87
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 85 SOLSNNSVSFFLYNLDHSHANYFCNLISFDPPPF--KVTLTGGLHIYESQLCCQLKFW 142
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 88 GKLGNESVTFYQLNLYVNQFTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLF- 146
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 143 LPICGAFFVVCILGCILC-----WTKRKYSSSVHDPNGEYMF 183
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 147 -PGPSKRFVWLVVVGVLACYSLLYTVAFIIFWVRSKR-SRLH---SDYNNM 194
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 10
US-08-505-058-3
; Sequence 3, Application US/08505058
; Patent No. 5773253
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Peach, Robert
; TITLE OF INVENTION: CTLA4 Mutant Molecules and Uses Thereof
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/505,058
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/228,208
; FILING DATE: 15-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.30US11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-505-058-3

Query Match          12.4%; Score 134; DB 1; Length 225;
Best Local Similarity 23.0%; Pred. No. 8e-08;
Matches 42; Conservative 32; Mismatches 77; Indels 32; Gaps 8;

QY 11 FCLRIVLTGEINGSANYEMFIFHNGVQILCKYPD--IVQQFMQLKGGQILCDLTKT 68
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
```


DB 12 FFXSVQVTENKILVKQSPLLYVDSNEVXSLSCRYSYNLLAKEFRASLYKG--VNSDVXEV 69
QY 69 -KSGGNVYSIKSLKF-----CHSOLSNNSVSFFLYNLDSHANYEFCNLSTFDPPPF--K 120
DB 70 CVGNGNFTYQOPQFRSNAEFNCDGDFDNETVTFRLMNLHVNHDTIYFCKIEFMYPPLXLDN 129
QY 121 VTLTGGYLIHYESQLC-----COLKFWLPIGCAAFVVCILGC-----ILICWLT 165
DB 130 ERSNGTIIHIKEKHLCHTXXXOSSPKLFW-----ALYVAVAGVLFVGLLVTAALCVIWTN 184
QY 166 KKK 168
DB 185 SRR 187

RESULT 11
US-08-459-818-23
; Sequence 23, Application US/08459818
; Patent No. 5851795
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damele, Nitin K.
; APPLICANT: Brady, William
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459, 818
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.35US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-818-23

Query Match 12.4%; Score 134; DB 2; Length 225;
Best Local Similarity 23.0%; Pred. No. 8e-08; Indels 32; Gaps 8;
Matches 42; Conservative 32; Mismatches 77;
QY 11 FCLRIRKVLTEGINGSANYEMFIHNGGVQILCKYPD--IVQOFKMOCLKGGQILCDLTKT 68
DB 12 FFXSVQVTENKILVKQSPLLYVDSNEVXSLSCRYSYNLLAKEFRASLYKG--VNSDVXEV 69
QY 69 -KSGGNVYSIKSLKF-----CHSOLSNNSVSFFLYNLDSHANYEFCNLSTFDPPPF--K 120
DB 70 CVGNGNFTYQOPQFRSNAEFNCDGDFDNETVTFRLMNLHVNHDTIYFCKIEFMYPPLXLDN 129
QY 121 VTLTGGYLIHYESQLC-----COLKFWLPIGCAAFVVCILGC-----ILICWLT 165
DB 130 ERSNGTIIHIKEKHLCHTXXXOSSPKLFW-----ALYVAVAGVLFVGLLVTAALCVIWTN 184

QY 166 KKK 168
DB 185 SRR 187

RESULT 12
US-08-889-666-23
; Sequence 23, Application US/08889666
; Patent No. 5885579
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damele, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889, 666
; FILING DATE: 08-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-889-666-23

Query Match 12.4%; Score 134; DB 2; Length 225;
Best Local Similarity 23.0%; Pred. No. 8e-08; Indels 32; Gaps 8;
Matches 42; Conservative 32; Mismatches 77;
QY 11 FCLRIRKVLTEGINGSANYEMFIHNGGVQILCKYPD--IVQOFKMOCLKGGQILCDLTKT 68
DB 12 FFXSVQVTENKILVKQSPLLYVDSNEVXSLSCRYSYNLLAKEFRASLYKG--VNSDVXEV 69
QY 69 -KSGGNVYSIKSLKF-----CHSOLSNNSVSFFLYNLDSHANYEFCNLSTFDPPPF--K 120
DB 70 CVGNGNFTYQOPQFRSNAEFNCDGDFDNETVTFRLMNLHVNHDTIYFCKIEFMYPPLXLDN 129
QY 121 VTLTGGYLIHYESQLC-----COLKFWLPIGCAAFVVCILGC-----ILICWLT 165
DB 130 ERSNGTIIHIKEKHLCHTXXXOSSPKLFW-----ALYVAVAGVLFVGLLVTAALCVIWTN 184
QY 166 KKK 168
DB 185 SRR 187

[illegible]

```

; Patent No. 5968510
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: Ctr14 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,776
; FILING DATE:
; CLASSIFICATION:
; PRIORITY INFORMATION:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-725-776-23

Query Match 12.4%; Score 134; DB 2; Length 225;
Best Local Similarity 23.0%; Pred. No. 8e-08;
Matches 42; Conservative 32; Mismatches 77; Indels 32; Gaps 8;

QY 11 FCLRIRKVLTEGINSANYEMFIHNGVQILCKYPD--IYQEFKQMLKGGQILCDLTKT 68
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 12 FFXSVOVTENKILVKQSPLLYVDNSNEVXSLSCRYSYNLAKFRASLYKG--VNSDVXEV 69

QY 69 -KSGSNTVSIKSLKF-----CHSQLSNNSVSFFLYNLDSHANYFCNLSIFDPPPF--K 120
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 CVGNGNFTYQOPFRSNAENCDGDFDNETVTFRILWNLHVNHHDIIYFCKIEFMYPPIYLDN 129
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 121 VTLTGVLHIVESQLC-----CQLKFWLPIGCAAFVVCILGC-----ILICWLT 165
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 ERSNGTIHIIKEKHLCHTXXXQSSPKLFW----ALYVAVGVLCFYGLLVTVALCVIWTN 184
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 166 KKK 168
; : :
Db 185 SRR 187

RESULT 15
US-08-488-062-23
; Sequence 23, Application US/08488062
; Patent No. 5977318
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.

```

APPLICANT: Brady, William
 APPLICANT: Kliener, Peter A.
 TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merchant & Gould
 STREET: 11150 Santa Monica Blvd., Suite 400
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/488,062
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/375390
 FILING DATE: 18-JAN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Adriano, Sarah B.
 REGISTRATION NUMBER: 34,470
 REFERENCE/DOCKET NUMBER: 30436-35US01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-445-1140
 TELEFAX: 310-445-9031
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 225 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-488-062-23

Query Match	12.4%;	Score 134;	DB 2;	Length 225;
Best Local Similarity	23.0%;	Pred. No. 8e-08;		
Matches 42;	Conservative 32;	Mismatches 77;	Indels 32;	Gaps 8;

QY 11 FCLRIRKVLTELGINGSANYEMFIHNGVQILCKYPD--IVQGRKMQLLKGQILCDLTKT 68
12 FFXSVQVTENKILVKKOSPLLYVDSDNEVXSLSCRYSYNLAKEFRAFLYKGG--VNSDVXEV 69
DB 69 -KSGSGNTVSISLSKF-----CHSQLSNNSVSFFLLYNLDHSHANYFCNLSTFDPDPF--K 120
70 CVGNGNFETYPQGRFNRNAEFNCDDGDFDNEFVTFRLMNLHVNHFTDLYFCKIEFMYPPPYLDN 129
QY 121 VTLTGGLHIYESQLC-----CQLKFWLPFGCAAFVNVCLIGC-----ILICWLT 165
DB 130 ERSNGTIIHIKEKHLCHTXXXQSSPKLEW-----ALYVAVAGVLEFCYGLLVYALCVIWTN 184
QY 166 KKK 168
DB 185 SRR 187

Search completed: October 21, 2002, 07:47:38
Job time : 16 secs

	Matches	44;	Conservative	30;	Mismatches	74;	Indels	25;	Gaps	7;
QY	30	MEIFHNGGVQILCKYPD-	IYQDFKMQLLKGQILCDLTKTKGSGN--	TVISIKSLKFCH	84					
Db	28	MLVAYDNAVNLSCKYSY	NLFSPREFRASLHKG	LDSAVEVCVYGYNSQ	OLQVYSKTGFCNC	87				
QY	85	SQLSNNVSFFLYNLDSH	SHANYFCNLSIFDPPPF--	KVTLTGGLHIE	SQLCCLKFW	142				
Db	88	GKLGNESVTFYQLNLY	NQTDIFYCKIEVMY	PPPLYLDNEKSN	GTIIHVKGKHLCP	SPLE-	146			
QY	143	LPICCAFWVVCILGCILIC	-----	WLTKKKYS	SVHDPNGEYFM	183				
Db	147	-PGPSKPFWALVVG	VLACYSLLVTVAFCIF	WMRSKR-SRL	LH--SDY	MNM	194			

RESULT 14			
ID	Q9BDN5	PRELIMINARY;	PRT; 220 AA.
AC	Q9BDN5;		
CS	01-JUN-2001 (TREMBLrel. 17, Created)		
CC	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
LN	CD28 PROTEIN.		
OS	Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;		
OX	Cercopithecinae; Cercopithecus.		
RN	NCBI_TaxID=9531;		
RP	[1]		
RA	SEQUENCE FROM N.A.		
RA	MEDLINE=21383618; PubMed=11491535;		
RA	Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,		
RT	Weiss W.R., Ansari A.A.;		
RT	"Cloning, sequencing, and homology analysis of nonhuman primate		
RL	Fas/Fas-ligand and co-stimulatory molecules.";		
DR	Immunogenetics 53:315-328(2001).		
DR	EMBL: AF344842; AAK37601.1; -.		
DR	HSSP; P16410; 1AH1.		
DR	InterPro: IPR003600; Ig_like.		
DR	SMART: SM00410; IG_like: 1.		
SO	SEQUENCE 220 AA; 25117 MW; 13BD03F7D937388F CRC64;		

Query Match	Similarity	12.58;	Score	135.5;	DB	6;	Length	220;
Best Local	44;	Conservative	30;	Mismatches	74;	Indels	25;	Gaps
								7;
QY	30	MEIFHNGVQILCKYPD--IVQQFKMQLKGGQILCDLTKTKSGN--TVSIKSLKFECH	84					
	28	MLVAYDNAVNLSCKSYTNLEFRASLHKGLDSAVEVCVYGNYSQOLQVYPKTFGNCD	87					
QY	85	SQLSNNVSSEFLYNLBDHSNANYEFCNLISFDPPE--KVPTLGGYLHIYESQACCOLKEFW	142					
Db	88	GKLGNESVTFYLONLVYNQTDIYFCKIEVMYPPPYLDNEKSNCTIITHVKGKHLCPSPLE-	146					
QY	143	LPIGCAAFVWVCILGCLIC-----WLTKKKYSVSHDPNGEYMMF	183					
Db	147	-PGPSKPFWALVVVGAGYACYSLLVTVAFRIEWMRSKR-SRLIH--SDYMMN	194					

```

RESULT 15
Q9BDM6
ID Q9BDM6 PRELIMINARY; PRT; 220 AA.
AC Q9BDM6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CD28 PROTEIN PRECURSOR.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]

```

RP	SEQUENCE FROM N.A.
RX	MEDLINE=21383618; PubMed=11491535;
RA	Vallinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RT	Weiss W.R., Ansari A.A.;
RL	"Cloning, sequencing, and homology analysis of nonhuman primate
DR	Fas/Fas-ligand and co-stimulatory molecules.";
DR	Immunogenetics 53:315-328(2001).
DR	EMBL; AF344855; AAK37538.1; -.
DR	HSSP; P16410; IAH1.
DR	InterPro; IPR003600; Ig_like.
DR	SMART; SM00410; IG_like; 1.
KW	Signal.
FT	SIGNAL. 1 18 POTENTIAL.
FT	VARIANT 34 34 N->S.
FT	VARIANT 70 70 E->G.
FT	VARIANT 71 71 D->N.
FT	VARIANT 83 83 E->G.
FT	VARIANT 122 122 Y->N.
FT	VARIANT 175 175 S->C.
FT	VARIANT 209 209 C->Y.
SO	SEQUENCE 220 AA; 25125 MW; 03776183006AE042 CRC64;

Query Match	12.18;	Score 130.5;	DB 6;	length 220;
Best Local Similarity	25.48;	Pred. No. 4.1e-06;		
Matches	44;	Conservative 28;	Mismatches 76;	Indels 25;
				Gaps 7;
QY	30	MEIFHNGVQILCKYPD--IVQOFKMOILKG---GQILCDLTKTKSGSNTVSIKSLKFCH	84	
Db	28	MLVAYDNAVNLSCKYSYNLFESREFRSLHKGGLDSAVEVCVYEDYSQQLQVYSKTEFNC	87	
QY	85	SQLSNNVSFELYNLDHSHANYFECNLISFDPPEF--KVYTLGGYLHIYESQOLCCQKFEW	142	
Db	88	GKLGNESVTFYQLNLVYNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHEKGKHLCPSPLE-	146	
QY	143	LPIGCAAFVVVVCILGICILC-----WLTKKKYSVSHDPNGEYMF	183	
Db	147	-PGPSKPFWALVVVGVGACYSLLVTVAFSIFWMSKR--SRLLH--SDYMM	194	

```
Search completed: October 21, 2002, 07:48:15
Job time : 32 secs
```

```
RA Yang S., Sam G., K.;  
RT "Nucleotide and Predicted Amino Acid Sequences of Canine CD28.";  
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF154842; AAG43370.1; -  
DR InterPro; IPR003600; IG_1like.  
DR SMART; SM00410; IG_1like; 1.  
KW Receptor.  
SQ SEQUENCE 221 AA; 25417 MW; 7BCE7EB595F66AFD CRC64;  
  
Query Match 13.0%; Score 140.5; DB 6; Length 221;  
Best Local Similarity 27.2%; Pred. No. 3.4e-07;  
Matches 46; Conservative 26; Mismatches 76; Indels 21; Gaps 9;  
  
QY 32 IFHNGVQILCKYPD--IVQQFKMQLLKGQILCDLTKTKG--SGNTVSIKSLKF-CHSQ 86  
DB 31 VVYNNEVNLCKYTYNLFKSKEFRASLYKGVDSAVEVCVNGNYSHPQFYSSSTGFDCDGK 90  
QY 87 LSNNVSFFLYNLDHSHANYFECNLSIFDPPPF--KVTLTGGLHIYESQLC-----C 137  
DB 91 LGNETVTFYLRNLEVNQTDIYFCKIEVMYPPYIGNEKSNGTIIHVKEKHLCPDELPPDS 150  
Q 138 QLKFW-LPIGCAAFVNVVLCILIC--WLTKKYSSSVHDPNGEYMF 183  
DB 151 SKPFWALVVGAVLVFYSLLVVALCAVWIKSK--SSRI--LQSDYMMN 195  
  
RESULT 11  
O9N0N8 PRELIMINARY; PRT; 221 AA.  
AC O9N0N8;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE T-CELL COSTIMULATORY MOLECULE CD28.  
GN CD28.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BREED BEAGLE;  
RX MEDLINE=21189496; Pubmed=11292534;  
RA Khatlani T.S., Ma Z., Okuda M., Onishi T.;  
RT "Molecular cloning and sequencing of canine T-cell costimulatory  
molecule (CD28).";  
RL Vet. Immunol. Immunopathol. 78:341-348(2001).  
DR EMBL; AF259962; AAF72533.1; -  
DT InterPro; IPR003600; IG_1like.  
L SMART; SM00410; IG_1like; 1.  
SL SEQUENCE 221 AA; 25364 MW; 0CCE7EB595EA1E3A CRC64;  
  
Query Match 13.0%; Score 140.5; DB 6; Length 221;  
Best Local Similarity 27.2%; Pred. No. 3.4e-07;  
Matches 46; Conservative 26; Mismatches 76; Indels 21; Gaps 9;  
  
QY 32 IFHNGVQILCKYPD--IVQQFKMQLLKGQILCDLTKTKG--SGNTVSIKSLKF-CHSQ 86  
DB 31 VVYNNEVNLCKYTYNLFKSKEFRASLYKGVDSAVEVCVNGNYSHPQFYSSSTGFDCDGK 90  
QY 87 LSNNVSFFLYNLDHSHANYFECNLSIFDPPPF--KVTLTGGLHIYESQLC-----C 137  
DB 91 LGNETVTFYLRNLEVNQTDIYFCKIEVMYPPYIGNEKSNGTIIHVKEKHLCPDELPPDS 150  
QY 138 QLKFW-LPIGCAAFVNVVLCILIC--WLTKKYSSSVHDPNGEYMF 183  
DB 151 SKPFWALVVGAVLVFYSLLVVALCAVWIKSK--SSRI--LQSDYMMN 195  
  
RESULT 12  
O28289 PRELIMINARY; PRT; 173 AA.  
ID O28289  
AC O28289;
```

```
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE CELL SURFACE PROTEIN (FRAGMENT).  
GN CD28.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BEAGLE;  
RX MEDLINE=94222451; Pubmed=8168859;  
RA Pastori R.L., Milde K.F., Alejandro R.;  
RT "Molecular cloning of the dog homologue of the lymphocyte antigen  
CD28.";  
RL Immunogenetics 39:373-373(1994).  
DR EMBL; L22178; AAA51453.1; -  
DR InterPro; IPR003600; IG_1like.  
DR SMART; SM00410; IG_1like; 1.  
FT NON_TER 1  
FT NON_TER 173  
SQ SEQUENCE 173 AA; 19770 MW; 7C265AE40931C1EA CRC64;  
  
Query Match 12.9%; Score 139.5; DB 6; Length 173;  
Best Local Similarity 26.8%; Pred. No. 3.3e-07;  
Matches 41; Conservative 24; Mismatches 71; Indels 17; Gaps 7;  
  
QY 32 IFHNGVQILCKYPD--IVQQFKMQLLKGQILCDLTKTKG--SGNTVSIKSLKF-CHSQ 86  
DB 12 VVYNNEVNLCKYTYNLFKSKEFRASLYKGVDSAVEVCVNGNYSHPQFYSSSTGFDCDGK 71  
QY 87 LSNNVSFFLYNLDHSHANYFECNLSIFDPPPF--KVTLTGGLHIYESQLC-----C 137  
DB 72 LGNETVTFYLRNLEVNQTDIYFCKIEVMYPPYIGNEKSNGTIIHVKEKHLCPDELPPDS 131  
QY 138 QLKFW-LPIGCAAFVNVVLCILIC--WLTKK 167  
DB 132 SKPFWALVVGAVLVFYSLLVVALCAVWIKSK 164  
  
RESULT 13  
Q9BDM8 PRELIMINARY; PRT; 220 AA.  
ID Q9BDM8  
AC Q9BDM8;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE CD28 PROTEIN PRECURSOR.  
OS Macaca nemestrina (Pig-tailed macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI_TaxID=9545;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21383618; Pubmed=11491535;  
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,  
RA Weiss W.R., Ansari A.A.;  
RT "Cloning, sequencing, and homology analysis of nonhuman primate  
Fas/Fas-ligand and co-stimulatory molecules.";  
RL Immunogenetics 53:315-328(2001).  
DR EMBL; AF344852; AAK37612.1; -  
DR HSSP; P16410; 1A1.  
DR InterPro; IPR003600; IG_1like.  
DR SMART; SM00410; IG_1like; 1.  
KW SIGNAL.  
FT SIGNAL. 1  
FT VARIANT 215  
FT VARIANT 215  
SQ SEQUENCE 220 AA; 24966 MW; 965F6D54DAF1AF0A CRC64;  
  
Query Match 12.6%; Score 136.5; DB 6; Length 220;  
Best Local Similarity 25.4%; Pred. No. 9.2e-07;
```

```
Db 131 GTVIHVKNNICPGVSPPEPKPFWTLVVFSGVIGVLSLSTMLLCVLTWKQRTRL--L 188
QY 177 NGEYMEM 183
Db 189 OSDYMMN 195

RESULT 7
O9N214
ID O9N214 PRELIMINARY; PRT; 221 AA.
AC - O9N214;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CD28.
GN
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
NCBI_TaxID=9685;
[1]
SEQUENCE FROM N.A.
RX MEDLINE-20094001; PubMed-10630305;
RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,
RA Mikami T., Takahashi E.;
RT "Molecular cloning and sequencing of a cDNA encoding the feline T-cell
RT antigen CD28 homologue."
RL Immunogenetics 50:369-370(1999).
DR EMBL; AB025316; BAA92349.1;
DR InterPro; IPR003600; Ig_like.
DR SMART; SM00410; Ig_like.1.
SO SEQUENCE 221 AA; 25283 MW; B17B76C52BA18DCB CRC64;

Query Match 13.4%; Score 145.5; DB 6; Length 221;
Best Local Similarity 28.3%; Pred. No. 9.8e-08;
Matches 45; Conservative 22; Mismatches 65; Indels 27; Gaps 8;

QY 32 IFHNGGVQILCKYPD--IVQQFKMQLKGGQILCDLTKTG--SGNTVSIKSLKF-CHSQ 86
Db 31 VVYNNEVNLSCKYTHNLFESKEFRASLYKGVDSAVEVCVNGNYSHQPFYSTGFDGDK 90

QY 87 LSNNVSFFLYNLDSHANYFCNLSIFDPPF--KVTLTGGLHIYESQLC-COLK-- 140
Db 91 LGNETVTFLRNLFVNQTDIFYCKIEVMYPPPYIDNEKSNGTIIHVKEKHLCPAQLSPES 150

QY 141 ---FWLPICGAFFVVCILG-----CILICWLTKKK 168
F 151 SKPFW----ALVVGCILGFYSLATVALGACWMKTKR 184

RESULT 8
O02757
ID O02757 PRELIMINARY; PRT; 221 AA.
AC O02757;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE T-CELL SPECIFIC SURFACE GLYCOPROTEIN CD28.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
[1]
SEQUENCE FROM N.A.
RP Hash S.M., Carpino M.R., Collisson E.W.;
RT "Felis catus t-cell specific surface glycoprotein CD28.";
RL Thesis (1996); Veterinary Pathobiology, Texas A&M Univ.
DR EMBL; U57754; AAB53574.1;
DR InterPro; IPR003600; Ig_like.
DR SMART; SM00410; Ig_like.1.
SO SEQUENCE 221 AA; 25317 MW; 5B71717E461AE5E3 CRC64;

Query Match 13.4%; Score 145.5; DB 6; Length 221;
```

```
Best Local Similarity 28.3%; Pred. No. 9.8e-08;
Matches 45; Conservative 22; Mismatches 65; Indels 27; Gaps 8;

QY 32 IFHNGGVQILCKYPD--IVQQFKMQLKGGQILCDLTKTG--SGNTVSIKSLKF-CHSQ 86
Db 31 VVYNNEVNLSCKYTHNLFESKEFRASLYKGVDSAVEVCVNGNYSHQPFYSTGFDGDK 90

QY 87 LSNNVSFFLYNLDSHANYFCNLSIFDPPF--KVTLTGGLHIYESQLC-COLK-- 140
Db 91 LGNETVTFLRNLFVNQTDIFYCKIEVMYPPPYIDNEKSNGTIIHVKEKHLCPAQLSPES 150

QY 141 ---FWLPICGAFFVVCILG-----CILICWLTKKK 168
Db 151 SKPFW----ALVVGCILGFYSLATVALGACWMKTKR 184

RESULT 9
O97630
ID O97630 PRELIMINARY; PRT; 219 AA.
AC O97630;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE T-CELL SPECIFIC SURFACE GLYCOPROTEIN CD28.
GN
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
[1]
SEQUENCE FROM N.A.
RX MEDLINE-99309828; PubMed-10380709;
RA Chaplin P.J., Pietrala L.N., Scheerlinck J.P.;
RT "Cloning and sequence comparison of sheep CD28 and CTLA-4.";
RL Immunogenetics 49:583-584(1999).
DR EMBL; AF092739; AAD04379.1;
DR InterPro; IPR003600; Ig_like.
DR SMART; SM00410; Ig_like.1.
SO SEQUENCE 219 AA; 25158 MW; D50AD339E5BC2327 CRC64;

Query Match 13.4%; Score 145; DB 6; Length 219;
Best Local Similarity 23.5%; Pred. No. 1.1e-07;
Matches 40; Conservative 35; Mismatches 75; Indels 20; Gaps 8;

QY 30 MFIHNGGVQILCKYPD--IVQQFKMQLKGGQILCDLTKTGS--GNTVSIKSLKF-CHS 85
Db 28 MLVVDNDEVNLSCKYTYNLFESKEFRASLYKGVDSAVEVCVNGNHSHPLOSTNKEFNCTV 87

QY 86 QLSNNSVSFFLYNLDSHANYFCNLSIFDPPF--KVTLTGGLHIYESQLC----- 136
Db 88 KVGNETVTFLQDLVYNQTDIFYCKLEVLVPPPYIDNEKSNGTIIHVKEKHLCPSPQSPPE 147

QY 137 COLKFWLPI--GCAAFVVCILGCIICWLTKKKYSSVHDPNGEYMEM 183
Db 148 SSKPFWALVVVNGVLFVYSLLVTVALCNCWMSKR--NRMH--OSDYMMN 193

RESULT 10
O9GKP3
ID O9GKP3 PRELIMINARY; PRT; 221 AA.
AC O9GKP3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE COSTIMULATORY MOLECULE B7 RECEPTOR CD28.
GN
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
[1]
SEQUENCE FROM N.A.
```


OY 64 DLTKTSGSNTVSIKSLKFCHSQLSNNSVSFFLYNLNDHSHANYFCNLSTFDDPPFKV-T 122
 Db 64 ELTKTGSSNAVASIKNPMLCTLHYLNNSNVSVFLNNPDSSQGSYYFCSLSIFDPPPQERN 123

OY 123 LTGGYLHIYESQLCCOLKFWLPICCAAFVVVCILGCIILCWLTKKKYSSVDHPNGEYM 182
 Db 124 LSGGYLIHIESQLCCOLKLWLPVGCAAFVVLLEGCILLIWFSKKKYGSSVDHPNSEYMF 183

OY 183 MRAVNATAKSRLTDVT 198
 Db 184 MAAVNTNKRSRLAGMT 199

RESULT 4
 O9RIT7 PRELIMINARY; PRT; 200 AA.
 ID O9RIT7;
 AC O9RIT7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE ACTIVATION-INDUCIBLE LYMPHOCTE IMMUNOMEDIATORY MOLECULE ALLIM RECURSOR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10116;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20462959; PubMed=11006126;
 RA Tezuka K., Tsuji T., Hirano D., Tamatani T., Sakamaki K., Kobayashi Y., Kamada M.;
 RT "Identification and characterization of rat Allim/iCOS, a novel T-cell costimulatory molecule, related to the CD28/CTLA4 family." ;
 RL Biochem. Biophys. Res. Commun. 276:335-345(2000).
 DR EMBL; AB023134; BAA82128.1; .
 FT SIGNAL.
 SQ SEQUENCE 1 20 POTENTIAL.
 22529 MW; OA74C35581FI29D4 CRC64;

Query Match 64.8%; Score 701; DB 11; Length 200;
 Best Local Similarity 67.9%; Pred. No. 5,4e+68;
 Matches 133; Conservative 17; Mismatches 42; Indels 4; Gaps 22,

OY 7 YE--FEECLRIRKVLTGEINGSANYEMEFIHNGGVQICKRPDIVOQFMOLLKGGOILC 63
 Db 4 YFSCEVFECFLIKLLTLGLDLNLANHRMSEPHDGVOISCNYPETVQQLMOLFKEKDREVL 63

OY 64 DLTKKTSGSNTVSIKSLKFCHSQLSNNSVSFFLYNLNDHSHANYFCNLSTFDDPPE-KVT 122
 Db 64 DLTKKTSGSNTVSIKNPMSCPYOLESNNNSVSFFLDNADSSOGSYELCSLSIFDPPPQEKN 123

OY 123 LTGGYLHIYESQLCCOLKFWLPICCAAFVVVCILGCIILCWLTKKKYSSVDHPNGEYM 182
 Db 124 LSGGYLIHIESQLCCOLKLWLPVGCAAFVAALLFGCIFIWFAKKKYRSSVDHPNSEYMF 183

OY 183 MRAVNATAKSRLTDVT 198
 Db 184 MAAVNTNKRSRLAGMT 199

RESULT 5
 O9WVR9 PRELIMINARY; PRT; 216 AA.
 ID O9WVR9;
 AC O9WVR9;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE ACTIVATION-INDUCIBLE LYMPHOCTE IMMUNOMEDIATORY MOLECULE ALLIM RECURSOR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_Taxid=10116;

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RX MEDLINE=20462959; PubMed=11006126;
RA Tezuka K., Tsuji T., Hirano D., Tamatani T., Sakamaki K.,
RA Kobayashi Y., Kamada M.;
RT "Identification and characterization of rat AILIM/ICOS, a novel T-cell
RT costimulatory molecule, related to the CD28/CTLA4 family.";
RL Biochem. Biophys. Res. Commun. 276:335-345(2000).
DR EMBL; AB023133; BAA82127.1; -.
RW Signal.
FT SIGNAL.
SQ SEQUENCE 216 AA; 24260 MW; 772E01320982B15A CRC64;

Query Match
Best Local Similarity 64.3%; Score 696; DB 11; Length 216;
Matches 132; Conservative 16; Mismatches 40; Indels 4; Gaps 2;

OY 7 YF---FLFCLRIKVLTEGINSANYEMFIHNGVQILCKYPDIVQOFKMOILKGQILC 63
   || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4 YFSCVFVFCFLIKLITGELNDLANHRMFSFHDGVOISCNYPETVQOLKMOLEKREVL 63

OY 64 DLTKTKSGNTVSIKSLKECHSOLSNSVSFFLYNLDSHANYFFCNLSIFDPPPF-KVT 122
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64 DLTTKGSGNTVSIKPNMPCPYQLSNNVSFFLDNADSSQGSYFLCSTLSTFDPPPFQEK 123

OY 123 LTGVLHIYESQLCCQLKFNLPICGAAFFVVCILGCLICWLTKKKYSSVHDNGEYMF 182
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 124 LSGVYLHIYESQLCCQLKFWLVPVCAAFVALLFGCIFIVMFAKKKYRSSVHDNSEYMF 183

OY 183 MRAVNTAKKSRL 194
   ||||| |||||
Db 184 MAAVNTNKKSR 195

RESULT 6
O9JLV4 PRELIMINARY; PRT; 221 AA.
ID O9JLV4
AC O9JLV4:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CD28 ANTIGEN.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
CX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RA Lu M., Yang D., Kemper T., Maier A., Rogendorf M.;
RT "Molecular characterization of woodchuck CD28 and cytotoxic T-
RT lymphocyte associated antigen 4 (CTLA-4).";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF130427; AAF36501.1; -.
DR InterPro; IPR003600; IG_1like.
DR SMART; SMO0410; IG_1like; 1.
SQ SEQUENCE 221 AA; 25594 MW; B29D32E987CE51D1 CRC64;

Query Match
Best Local Similarity 13.5%; Score 146.5; DB 11; Length 221;
Matches 43; Conservative 36; Mismatches 71; Indels 37; Gaps 7;

OY 14 RIKVLTGEINGSANYEMFIHNGVQILCKYPDIVQOFKMOILKGQILCDLTKTKSGN 73
   ||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 29 RLEIVNNEVNLCKKYTNLFS-----KEFRASLYKGVDSAYEVCVNGNFS 74

OY 74 TVSIKSLKF-----CHSOLSNSVSFFLYNLDSHANYFFCNLSIFDPPPF--KVTLT 124
   ||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 75 ----HQLQFYSHTGFCNCDKRLGNETVTFYLRNLVYNQTDIYFCKIEVMYPPPYLDNEKSN 130

OY 125 GGYLHIYESQLCCQL-----KFW-LPICGAAFFVVCILGCLICWLTKKKYSSVHDP 176
   ||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2002, 07:46:28 ; Search time 20 Seconds
(without alignments)
956.089 Million cell updates/sec

Title: US-09-823-307C-2
Perfect score: 1082
Sequence: 1 MKSGLMYFFLFCLRIKVLTC.....YMFMAVNTAKKSRLTDVTL 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Tc: number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1082	100.0	199	2	578540 inducible T-cell c
2	701	64.8	200	2	JC7397 activation-inducib
3	696	64.3	216	2	JC7396 activation-inducib
4	152	14.0	218	2	S24413 T-cell surface gly
5	150.5	13.9	221	2	I46689 CD28 precursor - r
6	139.5	12.9	173	2	I46197 cell surface prote
7	139.5	12.9	220	1	RWHU28 T-cell surface gly
8	138	12.8	218	2	A43523 T-cell surface gly
9	103.5	9.6	988	2	T18986 hypothetical prote
10	97	9.0	221	2	S25168 CHT28 protein - ch
11	91.5	8.5	383	2	T21946 hypothetical prote
12	87	8.0	330	2	A40071 Fc gamma (IgG) rec
13	87	8.0	330	2	I49660 Fc-gamma-1/gamma-2
14	87	8.0	563	2	T33479 hypothetical prote
15	86.5	8.0	223	2	A29063 cytotoxic T-lympho
16	86	7.9	223	2	T09536 cytotoxic T-lympho
17	84	7.8	283	1	FCMSG1 Fc gamma (IgG) rec
18	84	7.8	285	2	A26944 conserved hypotet
19	83.5	7.7	186	2	S08614 cytotoxic T-lympho
20	82.5	7.6	248	1	QOBE4L probable glycoprot
21	81	7.5	276	2	S20690 31.6k hypothetical
22	81	7.5	680	2	JC5895 killer cell inhibi
23	81	7.5	1584	2	S57161 hypothetical prote
24	80.5	7.4	247	2	D90028 hypothetical prote
25	80.5	7.4	635	2	JC5896 killer cell inhibi
26	78	7.2	231	2	T23136 hypothetical prote
27	77.5	7.2	80	2	F86027 hypothetical prote
28	77.5	7.2	220	2	A48581 37k proline-rich s
29	77.5	7.2	1070	2	JC4593 protein-tyrosine k

30	77	7.1	338	2	T34364 hypothetical prote
31	77	7.1	2104	2	D91286 hypothetical prote
32	77	7.1	2104	2	H86127 hypothetical prote
33	76.5	7.1	223	2	I46696 CTLA-4 precursor -
34	76.5	7.1	323	2	S06946 Fc gamma (IgG) rec
35	76.5	7.1	1237	2	A54080 protein-tyrosine-p
36	76	7.0	301	2	I54209 hypothetical prote
37	76	7.0	317	2	JL0118 Fc gamma (IgG) rec
38	76	7.0	546	2	S52053 cytochrome-c oxida
39	75.5	7.0	261	2	S29360 Fc gamma (IgG) rec
40	75.5	7.0	277	2	T21330 hypothetical prote
41	75.5	7.0	2135	2	T14602 variant-specific s
42	75	6.9	418	2	AD3417 transporter, mfs s
43	75	6.9	1132	1	OSBPL host specificity p
44	74.5	6.9	201	2	G90134 hypothetical prote
45	74.5	6.9	235	2	I50610 T-cell surface gly

ALIGNMENTS

RESULT 1

S78540 inducible T-cell co-stimulator ICOS precursor - human
C/Species: Homo sapiens (man)
C/Date: 05-Mar-1999 #sequence_#revision 05-Mar-1999 #text_change 07-May-1999
C/Accession: S78540; S78748; S78749
R/Kroczeck, R.
Submitted to the Protein Sequence Database, June 1998
A/Reference number: S78540
A/Accession: S78540
A/Molecule type: mRNA
A/Residues: 1-199 <KRO>
A/Experimental source: cell line MOLT-4V
R/Hutloff, A.; Dittlich, A.M.; Beler, K.C.; Eljaschewitsch, B.; Kraft, R.; Anagnostop
Nature 397, 263-266, 1999
A/Title: ICOS is an inducible T-cell co-stimulator structurally and functionally rela
A/Reference number: S78748; MUID:99127892
A/Accession: S78748
A/Molecule type: mRNA
A/Residues: 1-199 <HUT1>
A/Experimental source: cell line MOLT-4V
A/Accession: S78749
A/Molecule type: protein
A/Residues: 'X', 193-198 <HUT2>
A/Experimental source: cell line MOLT-4V
C/Complex: homodimer
C/Superfamily: immunoglobulin homology
C/Keywords: dimer; glycoprotein; T-cell; transmembrane protein
F:1-19/Domain: (or 1-20) signal sequence #status predicted <SIG>
F:20-199/Product: (or 21-199) inducible costimulator ICOS #status predicted <EXT>
F:21-138/Domain: extracellular #status predicted <EXT>
F:26-132/Domain: immunoglobulin homology <IMM>
F:139-164/Domain: transmembrane #status predicted <TMM>
F:165-199/Domain: intracellular #status predicted <INT>
F:23,89,110/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 1082; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.1e-97;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKSGLMYFFLFCLRIKVLTCGEINGSANYEMFIHNGVQILCKYPDIVOQFKMQLKGGQ	60
DB	1	MKSGLMYFFLFCLRIKVLTCGEINGSANYEMFIHNGVQILCKYPDIVOQFKMQLKGGQ	60
QY	61	ILCDLTKTKGSGNTVSISLKFCHSOLSNNSVSFFLYNLDSHANYFCNLSIFDPPPFK	120
DB	61	ILCDLTKTKGSGNTVSISLKFCHSOLSNNSVSFFLYNLDSHANYFCNLSIFDPPPFK	120
QY	121	VTLTGGLHYEESQLCCQLKFWLPIGCAAFVVCILGICILCKKYSVHDNGEY	180
DB	121	VTLTGGLHYEESQLCCQLKFWLPIGCAAFVVCILGICILCKKYSVHDNGEY	180

QY 181 MEMRAVNTAKKSRLTDVTL 199
 Db 181 MEMRAVNTAKKSRLTDVTL 199

RESULT 2

activation-inducible lymphocyte immuno-mediatory molecule-2 - rat

JC7397

C/Species: Rattus norvegicus (Norway rat)

C/Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 17-Nov-2000

C/Accession: JC7397; PC7100

R;Tezuka, K.; Tsuji, T.; Hirano, D.; Tamatani, T.; Sakamaki, K.; Kobayashi, Y.; Kamada, Biochem. Biophys. Res. Commun. 276, 335-345, 2000

A/Title: Identification and characterization of rat ALLIM/ICOS, a novel T-cell costimula

A/Reference number: JC7396

A/Contents: Spleen

A/Accession: JC7397

A/Molecule type: mRNA

A/Residues: 1-200 <TE2>

Cross-references: DDBJ:AB023134

Accession: PC7100

A/Molecule type: protein

A/Residues: 21-40 <TE2>

C/Comment: This protein is an inducible cell surface glycoprotein, and a type I transmem

on, and plays an important role for the maturation or selection of T cells in thymus.

C/Genetics:

A/Gene: allim-2

C/Keywords: glycoprotein; T-cell; transmembrane protein

Query Match 64.8%; Score 701; DB 2; Length 200;

Best Local Similarity 67.9%; Pred. No. 2.2e-60;

Matches 133; Conservative 17; Mismatches 42; Indels 4; Gaps 2;

QY 7 YF--FLFCLRIKVLTEINGSANTEMFIFHNGGVQILCKYPDIVOQFKMQLKGGQILC 63

Db 4 YFSCVFVFCFLIKLTLGELNDLANHRMFESHGQVQISCNYPETVQOLKMQLFKDRVLC 63

QY 64 DLTKTSGSNTVSISLKFCHSOLSNSVSFFLYNLDSHANYFCNLSIFDPPPF-KVT 122

Db 64 DLTKTSGSNTVSISLKNPMSCPYQLSNNVSFFLDNADSSQGSYFLCSLIFDPPPFQEK 123

QY 123 LTGGYLHIYESQLCCQLKFWLPFGCAAFVVCILGCLICWLTKKKYSSSVHDPNGEYMF 182

Db 124 LSGGYLLIYESQLCCQLKFWLPVGCFAAFVALLFGCIFIWPAKKYRSSVHDPNSEYMF 183

QY 183 MRAVNTAKKSRLTDVT 198

Db 184 MAAVNTNKKSRLAGMT 199

RESULT 3

activation-inducible lymphocyte immuno-mediatory molecule-1 - rat

JC7396

C/Species: Rattus norvegicus (Norway rat)

C/Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 17-Nov-2000

C/Accession: JC7396; PC7099

R;Tezuka, K.; Tsuji, T.; Hirano, D.; Tamatani, T.; Sakamaki, K.; Kobayashi, Y.; Kamada, Biochem. Biophys. Res. Commun. 276, 335-345, 2000

A/Title: Identification and characterization of rat ALLIM/ICOS, a novel T-cell costimula

A/Reference number: JC7396

A/Contents: Spleen

A/Accession: JC7396

A/Molecule type: mRNA

A/Residues: 1-216 <TE2>

A/Cross-references: DDBJ:AB023133

A/Accession: PC7099

A/Molecule type: protein

A/Residues: 21-40 <TE2>

C/Comment: This protein is an inducible cell surface glycoprotein, and a type I transmem

on, and plays an important role for the maturation or selection of T cells in thymus.

C/Genetics:

A/Gene: allim-1

C/Keywords: glycoprotein; T-cell; transmembrane protein

Query Match 64.3%; Score 696; DB 2; Length 216;
 Best Local Similarity 68.8%; Pred. No. 7.3e-60;
 Matches 132; Conservative 16; Mismatches 40; Indels 4; Gaps 2;

QY 7 YF--FLFCLRIKVLTEINGSANTEMFIFHNGGVQILCKYPDIVOQFKMQLKGGQILC 63

Db 4 YFSCVFVFCFLIKLTLGELNDLANHRMFESHGQVQISCNYPETVQOLKMQLFKDRVLC 63

QY 64 DLTKTSGSNTVSISLKFCHSOLSNSVSFFLYNLDSHANYFCNLSIFDPPPF-KVT 122

Db 64 DLTKTSGSNTVSISLKNPMSCPYQLSNNVSFFLDNADSSQGSYFLCSLIFDPPPFQEK 123

QY 123 LTGGYLHIYESQLCCQLKFWLPFGCAAFVVCILGCLICWLTKKKYSSSVHDPNGEYMF 182

Db 124 LSGGYLLIYESQLCCQLKFWLPVGCFAAFVALLFGCIFIWPAKKYRSSVHDPNSEYMF 183

QY 183 MRAVNTAKKSRL 194

Db 184 MAAVNTNKKSR 195

RESULT 4

S24413

T-cell surface glycoprotein CD28 - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C/Accession: S24413; S38722

R;Clark, G.J.; Dallman, M.J.

Immunogenetics 35, 54-57, 1992

A/Title: Identification of a cDNA encoding the rat CD28 homologue.

A/Reference number: S24413; MUID:92104640

A/Accession: S24413

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-218 <CL>

A/Cross-references: EMBL:X55288

R;Clark, G.J.; Dallman, M.J.

submitted to the EMBL Data Library, October 1990

A/Reference number: S38722

A/Accession: S38722

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-152, 'P', 154-218 <CL2>

A/Cross-references: EMBL:X55288; NID:955905; PIDN:CAA39003.1; PID:955906

C/Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology

C/Keywords: glycoprotein

F;34-115/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 14.0%; Score 152; DB 2; Length 218;

Matches 42; Conservative 25; Mismatches 65; Indels 28; Gaps 7;

QY 30 MFIHNGVOILCKYPD--IVQOFKMLKGGQILCDLTKTSGSNTVSISLK-----F 82

Db 29 LTVVDNNEVSLSCRYSYNLAKERASLYKG--VNSDVEVCVGNFVQDFRPNVGFN 86

QY 83 CHSOLSNSVSFFLYNLDSHANYFCNLSIFDPPPF--KVTLTGGYLHIYESQLC--- 136

Db 87 CDGNEDETFTVTRLWNLVDVNHDTIYFCKIEVMYPPYLDNEKSNGTIIHKEKHLCHAQT 146

QY 137 COLKFWLPFGCAAFVVCILG-----ILICWLTKKK 168

Db 147 SPKLFW-----ALVVAVAGVLCYGLLVTVTLCIWTNSR 181

RESULT 5

I46689

CD28 precursor - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 21-Jan-2000

C/Accession: I46689

R;Isono, T.; Seto, A.

Immunogenetics 42: 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule
A:Reference number: I46689; MUID:95369849
A:Accession: I46689
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-221 <ISO>
A:Cross-references: GB:D49841; MID:g755094; PIDN:BAA08641.1; PID:g755095
C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
E:34-115/Domain: immunoglobulin homology <IM>

Query Match	Similarity	Score	DB 2	Length
Best Local	23.8%	150.5	4e-07	221
Matches	38	Conservative	27	Mismatches 70; Indels 25; Gaps 6;
OY	30	MEIFHNGVQILCKYPD--IVQOFKMOILKGQILCDLTTKGS-----GNTVSIKSL	80	
Db	29	MLVYNNNENLSCKYTYNLFSEKPERASLYKGADSAVECVVNGNFSHPHOHSTGTGN--	86	
OY	81	KFCHSOLSNNSVSFFLYNLDSHANYEFCNLSTFDPPEF--KVTLTGGYLYHYESQLC--	136	
DI	87	--CDGRIGNETVTFFYLNLYNOTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKEQHFCPA	144	
OY	137	-----COLKFWLPI--GCAAFVVCILGICILICWLTKKK	168	
Db	145	HPSPKSSTLFWLVVVGAVLAFYSMLVTVALFSCWMSKK	184	

RESULT 6
I46197
cell surface protein - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I46197
R:Pastori, R.L.; Milde, K.F.; Alejandro, R.
I:Immunogenetics 39, 373, 1994
A:Title: Molecular cloning of the dog homologue of the lymphocyte antigen CD28.
A:Reference number: I46197; MUID:94222451
A:Accession: I46197
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-173 <PAS>
A:Cross-references: GB:L22178; NID:g510693; PIDN:AAA51453.1; PID:g510694
C:Genetics:
A:Gene: CD28
C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
F:15-96/Domain: immunoglobulin homology<IMM>

```

every Match      12.98; Score 139.5; DB 2; Length 173;
: Local Similarity 26.8%; Pred. No. 3.9e-06;
: ches 41; Conservative 24; Mismatches 71; Indels 17; Gaps 7;

QY 32 IFHNGVOILCKYPD--IYQOFKMOILKGQILCDLTKTKG--SGNTVSIKSLKF-CHSQ 86
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 12 VVYNNEENLSCKYTYNLSFNEFRASLYKGVDSAVECVVNGNYSHPQFYSSSTGFDCDGK 71

QY 87 LSNNSVSFEFLYNLDHSHANYEFCNLSEIDPPPF--KVTLTGGYLHIYESQLC-----C 137
   | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 72 LGENEYTFYLRNLFEVNGTIDYLFCKIEVMYPPPYIGNEKSNGTIIHVKERKHLCPDELFPPDS 131

QY 138 QLKFW-LPIGCAAFVNVVCILGCILIC--WLTKK 167
   | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 132 SKPEWALVVGVAVLVFVYSLTLVTVALCAAYIKSK 164

```

RESULT 7
RWMU28
T-cell surface glycoprotein CD28 precursor - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999
C:Accession: A39983; A45895
R:Aruffo, A.; Seed, B.
Proc. Natl. Acad. Sci. U.S.A. 84, 8573-8577, 1987

A:Title: Molecular cloning of a CD28 cDNA by a high-efficiency COS cell expression system
A:Reference number: A39983; MUID:88068631
A:Accession: A39983
A:Molecule type: mRNA
A:Residues: 1-220 <ARU>
A:Cross-references: GB:J02988; NID:g338444; PIDN:AAA60581.1; PID:g338445
R:Lee, K.P.; Taylor, C.; Petryniak, B.; Turka, L.A.; June, C.H.; Thompson, C.B.
J. Immunol. 145, 344-352, 1990
A:Title: The genomic organization of the CD28 gene. Implications for the regulation of
T-cell activation
A:Reference number: A45895; MUID:90293482
A:Accession: A45895
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 35-134 <LEE>
A:Cross-references: GB:M37813
C:Genetics:
A:Gene: GDB:CD28
A:Cross-references: GDB:118765; OMIM:186760
A:Map position: 2q33-2q34
A:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C:Keywords: glycoprotein; homodimer; T-cell; transmembrane protein
F:1-18/Domain: signal sequence #status predicted <Sig>
F:19-220/Product: T-cell surface glycoprotein CD28 #status predicted <Mat>
F:19-152/Domain: extracellular #status predicted <Ext>
F:33-114/Domain: immunoglobulin homology <Imm>
F:153-179/Domain: transmembrane #status predicted <TMM>
F:180-220/Domain: intracellular #status predicted <INT>
F:71,92,105,129/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	12.9%;	Score 139.5;	DB 1;	Length 220;
Best Local Similarity	26.0%;	Pred. No. 5,1e-06;		
Matches 45;	Conservative 30;	Mismatches 73;	Indels 25;	Gaps 7;
QY	30	MEIFHNGVQILCKYPD--IVQQFKMQLKGGQILCDLTTKTSGSN--TVSIKSLKFC	84	
DB	28	MLVAYDNADVNLSCKSYNLFSEHFRASLHKGLDGAIVECVVYGNYSQQLYYSKTGFNCD	87	
QY	85	SQLSNNSVSFFLYNLDSHANYVFCNLSIFDPPPF--KVLTGTGYLHIYESQLCCQLKFW	142	
DB	88	GKLGNESVTFFYLONLYVNQTDIIYFCKIEVMYPPPIYDNEKSNGTIIHVKGKHLCPSPLF-	146	
QY	143	LPIGCAAFVVCVILGCLIC-----WLTKKYSSSVHDPNGEYFEM	183	
DB	147	-PGPSKPFVVLVVGGVLAQSLLVTVAFIIIFWRSKR-SRL/LH--SDYNNM	194	

RESULT 8
A43523
T-cell surface glycoprotein CD28 homolog precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 23-Jul-1999
C:Accession: A43523
R:Gross, J.A.; St. John, T.; Allison, J.P.
J. Immunol. 144, 3201-3210, 1990
A:Title: The murine homologue of the T lymphocyte antigen CD28. Molecular cloning and
A:Reference number: A43523; MUID:90217534
A:Accession: A43523
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-218 <GRO>
A:Cross-references: GB:M34563; NID:g192482; PIDN:AAA37395.1; PID:g309157
C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
;Keywords: glycoprotein; transmembrane protein

Query Match	12.8%	Score 138;	DB 2;	Length 218;
Best Local Similarity	24.4%;	Pred. No. 7e-06;	Mismatches 28;	Gaps 7;
Matches	39;	Conservative	26;	Indels
OY	30	MEFTHNGVQILCKYPD--IVQQFKMQLKGGQILCDLTKTGSGNIVSIKSLKF-----	82	
	:	: : : : : :	:	
	:	: : : : : :	:	
	:	: : : : : :	:	
Db	29	LTVDSNEVSLSRCRYNLAKERASLYKG--VNSDVEVCVGNGNFVTQPQRSNAEFN	86	
OY	83	CHSOLSNNSVSFFLYLNIDHSHANYFCNLISFDPPPF--KVTLGGGYLIHYEQLC---	136	

```
Db      87 CDGDPDNETVTERLWNLHVHHTDIYFCKIEFMYPPLDNEBSNGTIIHKEKHLCHTOS 146
QY      137 CQLKFWLPICGAFAVVCILGC-----ILICWLTKKK 168
Db      147 SPKLEW-----ALVAVAGVLEFCYGLLVLTVALCVMTNSRR 181

RESULT 9
T18986
hypothetical protein C06B3.11 - Caenorhabditis elegans
C:/Species: Caenorhabditis elegans
C:/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:/Accession: T18986
R:/Percy, C.
submitted to the EMBL Data Library, July 1996
A:/Reference number: Z19056
A:/Accession: T18986
A:/Status: preliminary; translated from GB/EMBL/DBDJ
Molecule type: DNA
Residues: 1-988 <WIL>
A:/Cross-references: EMBL:Z77652; PIDN:CAB01120.1; GSPDB:GN00023; CESP:C06B3.11
A:/Experimental source: clone C06B3
A:/Gene: CESP:C06B3.11
A:/Map position: 5
A:/Introns: 21/3; 75/2; 124/2; 150/1; 204/3; 239/2; 274/1; 330/3; 366/3; 407/1; 441/2; 54

Query Match
Best Local Similarity 23.0%; Score 103.5; DB 2; Length 988;
Matches 55; Conservative 29; Mismatches 74; Indels 81; Gaps 12;

QY      6 WYFPLECLRIKVL-----GEINGSANYEMFIHNG-----VQILCK 43
Db      324 WYCFAPSMLLTVMILPFESACAGSFDYLLFAFRSGCPKVMITQFLASYFWIVPVCM 383
QY      44 YPDIVQCFKMOL--LKGGIILCDLTKTKSGNTVS-----IKSLKFSHLSNNS 91
Db      384 VLNIILIFHMSLSKKNKM-----SONSASARQAQERRLIQSIALTTFILSHEI 434
QY      92 VSF-----FLYNLDHSHANYF-----CNLSIFDPPPFKVTL-TGGLHIYESQ 134
Db      435 ASFTLELFLPEIFSYFLDNGTFLYFIFSHDYVCSMYEFNTDDFSVHLQTKRYL-IQDPS 493
QY      135 L---CCQLKFWLPICGAFAVVCILGCI-----LICWLTKKKYSSSVHDPNGEYMF 183
Db      494 LEIKSCKFPDQLPVVYIYLMACISIGCCFVEFOSDIIPYFMKRK-----AYMMW 542

RESULT 10
S25168
CHT28 protein - chicken
C:/Species: Gallus gallus (chicken)
C:/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:/Accession: T50619; S25168
R:/Young, J.R.; Davison, T.F.; Tregaskes, C.A.; Rennie, M.C.; Vainio, O.
J. Immunol. 152, 3848-3851, 1994
A:/Title: Monomeric homologue of mammalian CD28 is expressed on chicken T cells.
A:/Reference number: T50619; MUID:94194147
A:/Accession: T50619
A:/Status: preliminary; translated from GB/EMBL/DBDJ
A:/Molecule type: mRNA
A:/Residues: 1-221 <Y02>
A:/Cross-references: EMBL:X67915; NID:g63221; PIDN:CAA48114.1; PID:g63222
C:/Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C:/Keywords: transmembrane protein

Query Match
Best Local Similarity 22.8%; Score 97; DB 2; Length 221;
Matches 41; Conservative 27; Mismatches 78; Indels 34; Gaps 9;

QY      26 ANYEMFIHNGVQILCKYP--DIVQCFKMQLKGGQ-----ILCDLTKTKSGNTVS 76
```

```
Db      24 AQRPLIVANRATLVCNNTYNGTGKEFRASLHKGTDSAVEVCISWMMTKINSNSK-- 81
QY      77 IKSLKF-CHSOLSNNSVSFFLYNLDHSHANYFECNLSIFDPP--FKVTLTGGLHIYES 133
Db      82 ----EFNCRGIDKDKVIFNLMMNSASQTDIYFCKIEAMYPYPVYNEKSNGTIVHRET 137
QY      134 QLCCQ----LKFWLPI--GCAFAVVCILGICILCWLTKK--KYSSSVHDPNGEYMF 183
Db      138 PIQTQEPESATSYWVAVTGLGFIYSLITAVFIITRYOKSKRNRYROS-----DYMMN 191

RESULT 11
T21946
hypothetical protein F38B2.3 - Caenorhabditis elegans
C:/Species: Caenorhabditis elegans
C:/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:/Accession: T21946
R:/Kershaw, J.
submitted to the EMBL Data Library, July 1995
A:/Reference number: Z19492
A:/Accession: T21946
A:/Status: preliminary; translated from GB/EMBL/DBDJ
A:/Molecule type: DNA
Residues: 1-383 <WIL>
A:/Cross-references: EMBL:Z50045; PIDN:CAA90363.1; GSPDB:GN00028; CESP:F38B2.3
A:/Experimental source: clone F38B2
A:/Gene: CESP:F38B2.3
A:/Map position: X
A:/Introns: 21/1; 52/1; 135/2; 184/1; 226/2; 260/2; 299/1; 359/2

Query Match
Best Local Similarity 23.6%; Score 91.5; DB 2; Length 383;
Matches 38; Conservative 23; Mismatches 51; Indels 49; Gaps 8;

QY      43 KYPDIVQCFKMQLKGGQILCD--LTKTKSGNTVSISKSLKFSHLSNNSVSFFLYNLD 100
Db      240 KYHDFLK-----YDGNSTIDPIITRISQENYVTIN-----STSNILFFEMTD 284
QY      101 HS-----HANYFECNLSIFDPPPFKVTLTGGLHIYESQLCCQLKFWLPICGAFAVVC 154
Db      285 ESNNGKGYHANYF-----ARPMTIDHTLGETH-----WIVLICVAFLTYP 324
QY      155 ILGICILCWLTKK--KYSSSVHDPNGEYMFRA--VNTA 189
Db      325 MIAGVIYFVIRKKNHROLESLNHPITISYSSSEAGSSINIA 365

RESULT 12
A40071
Fc gamma (IgG) receptor II (low affinity) beta (splice form 1) precursor - mouse
C:/Species: Mus musculus (house mouse)
C:/Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 23-Jul-1999
C:/Accession: A40071; A60761; S29361
R:/Hogarth, P.M.; Wilfort, E.; Hulet, M.D.; Bonnerot, C.; Even, J.; Fridman, W.H.; McI
J. Immunol. 146, 369-376, 1991
A:/Title: Structure of the mouse betaFc gamma receptor II gene.
A:/Reference number: A40071; MUID:91079576
A:/Accession: A40071
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-330 <HOG>
A:/Cross-references: GB:M63284; NID:g192161; PIDN:AAA37289.1; PID:g192163
R:/Ish, M.; Quelch, K.; Deacon, N.J.; McKenzie, I.F.C.; Hogarth, P.M.
Immunogenetics 31, 202-206, 1990
A:/Title: Identification of the mouse beta Fc gammaRII polymorphism by direct sequencin
A:/Reference number: A60761; MUID:90202030
A:/Accession: A60761
A:/Status: preliminary; nucleic acid sequence not shown; translation not shown
A:/Molecule type: mRNA
A:/Residues: 1-144, 'P', 146-189, 'Q', 191-298, 'P', 300-330 <LAH>
A:/Cross-references: GB:M31312; NID:g193260; PIDN:AAA37610.1; PID:g387155
R:/Raveitch, J.V.; Luster, A.D.; Weinstein, R.; Kochan, J.; Pavlovic, A.; Portnoy, D.A.
```


Science 234, 718-725, 1986
A:Title: Structural heterogeneity and functional domains of murine immunoglobulin G Fc
A:Reference number: S29360; MUID:87042761
A:Accession: S29361
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-269, 'L', 271, 'A', 'CQ', 276, 'RA', 279-330 <RAV>
A:Cross-references: EMBL:M16367; NID:g193256; PIDN:AAA37608.1; PID:g309230
C:Superfamily: Fc gamma receptor IIT; immunoglobulin homology
C:Keywords: immunoglobulin receptor
F:1-29/Domain: signal sequence #status predicted <SIG>
F:50-101/Domain: immunoglobulin homology <IMM1>
F:131-184/Domain: immunoglobulin homology <IMM2>

Query Match 8.0%; Score 87; DB 2; Length 330;
Best Local Similarity 20.4%; Pred. No. 0.95;
Matches 44; Conservative 29; Mismatches 53; Indels 90; Gaps 11;

OY 33 FHNG---GVQILCKYPDIYQFKMQLKGGQILCDLTKTKGS-----71
Df 71 FHNGRSIRSQVQASY-----TFKATVNDSGEYRCQMEQTRLSDPVDLGVISDWLLQTPQ 125
OY 72 -----GNTVSIKSLKFCQSLSN--NSVSFF-----LYNLDHSHANYE 108
Db 126 LVFLEGETITLR---CHSWRNKLLNRISFFHNKESVRYHHYSSNFSIPKANSHSGDY 181
OY 109 CNLS---IFDPPRFKVTLTGGLHYESQLCCQLKFWLPI-----GCAAFVVCIL 156
Db 182 CKGSLGRTLHOSKPVTTIYQGP-----KSSRSLPVLTIYAAVTGIAVAATVITL 230
OY 157 GCILICWLTKKKYSSSVHDPN-----GEY 180
Db 231 --VSLVYLKKKQVPALPGNPDHREMGETLPEVEGEY 264

RESULT 13

I49660
Fc-gamma-1/gamma-2bR receptor precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C:Accession: I49660
R:Hogarth, P.M.; Hibbs, M.L.; Bonadonna, L.; Scott, B.M.; Witort, E.; Pietersz, G.A.; Mo
immunogenetics 26, 161-168, 1987
A:Title: The mouse Fc receptor for IgG (Ly-17): Molecular cloning and specificity.
A:Reference number: I49660; MUID:87306729
A:Accession: I49660
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-330 <RES>
C:Cross-references: GB:M17515; NID:g193254; PIDN:AAA37607.1; PID:g309229
C:Superfamily: Fc gamma receptor IIT; immunoglobulin homology
C:Keywords: immunoglobulin receptor
F:131-184/Domain: immunoglobulin homology <IMM>

Query Match 8.0%; Score 87; DB 2; Length 330;
Best Local Similarity 20.4%; Pred. No. 0.95;
Matches 44; Conservative 29; Mismatches 53; Indels 90; Gaps 11;

OY 33 FHNG---GVQILCKYPDIYQFKMQLKGGQILCDLTKTKGS-----71
Db 71 FHNGRSIRSQVQASY-----TFKATVNDSGEYRCQMEQTRLSDPVDLGVISDWLLQTPQ 125
OY 72 -----GNTVSIKSLKFCQSLSN--NSVSFF-----LYNLDHSHANYE 108
Db 126 LVFLEGETITLR---CHSWRNKLLNRISFFHNKESVRYHHYSSNFSIPKANSHSGDY 181
OY 109 CNLS---IFDPPRFKVTLTGGLHYESQLCCQLKFWLPI-----GCAAFVVCIL 156
Db 182 CKGSLGRTLHOSKPVTTIYQGP-----KSSRSLPVLTIYAAVTGIAVAATVITL 230
OY 157 GCILICWLTKKKYSSSVHDPN-----GEY 180
Db 231 --VSLVYLKKKQVPALPGNPDHREMGETLPEVEGEY 264

RESULT 14
T32479
hypothetical protein F52H2.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 02-Jun-2000
C:Accession: T32479
R:Chisoe, S.; Hawkins, J.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid F52H2.
A:Reference number: Z21175
A:Accession: T32479
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-563 <CH1>
A:Cross-references: EMBL:AF026214; PIDN:AAB71312.1; GSPDB:GN00028; CESP:F52H2.2
A:Experimental source: strain Bristol N2; clone F52H2
C:Genetics:
A:Gene: CESP:F52H2.2
A:Map position: X
A:Introns: 20/3; 60/1; 123/2; 162/1; 204/1; 255/2; 296/3; 329/1; 401/2; 433/3; 544/1
C:Superfamily: arginine permease

Query Match 8.0%; Score 87; DB 2; Length 563;
Best Local Similarity 24.1%; Pred. No. 1.7;
Matches 52; Conservative 24; Mismatches 58; Indels 82; Gaps 12;

OY 8 FFLCLRIRYLTGEINGSANYEMFIHNGVQI--LCKYPDIYQFKMQLK-----G 58
Db 305 WFAFCMPIFVACSTI-GSAN-----GVILTRLGSRDYROAIAEVAEPQPKIFG 354
OY 59 GQILCDLTKTKGSGNTVSIKSLKFC-----SOLSNSVSFFLYNLDHSHANYFC 109
Db 355 NRQLPNLTSQKIFGN---RLPREFNEFVEIIFLSALEKSMVVEFFYS-----ETLEFC 405
OY 110 -----NLIFDPPRFKVTLTG---GYL---HIYESQLCCQLKFWLPIGC 147
Db 406 GAREGOMPVNLTMVNKTTPIP-AVILTGLLSLYLLSNNTYSLINYIOVSYWAIIG 464
OY 148 A-----AFVVCILGIL 161
Db 465 AILALFYFRKTMPPDAPRAVKAPIVPIIFETIGCVLL 500

RESULT 15

A29063
cytotoxic T-lymphocyte protein 4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 05-Nov-1999
C:Accession: A29063; I49622
R:Bruneet, J.F.; Denizot, F.; Luciani, M.F.; Roux-Dosseto, M.; Suzan, M.; Mattei, M.G.
Nature 328, 267-270, 1987
A:Title: A new member of the immunoglobulin superfamily--CTLA-4.
A:Reference number: A29063; MUID:87258259
A:Accession: A29063
A:Molecule type: mRNA
A:Residues: 1-223 <BRU>

A:Cross-references: GB:X05719; NID:g50592; PIDN:CAA29191.1; PID:g50593
R:Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.
J Immunol. 147, 1037-1044, 1991
A:Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both m
A:Reference number: I49584; MUID:91318145
A:Accession: I49622
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-36 <RES>
A:Cross-references: GB:M74362; NID:g192833; PIDN:AAA37489.1; PID:g553903
C:Genetics:
A:Gene: Ctla-4
A:Map position: 1, band C
C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C:Keywords: transmembrane protein

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2002, 07:46:28 ; Search time 12 seconds
(without alignments)
642.099 Million cell updates/sec

Title: US-09-823-307C-2
Perfect score: 1082
Sequence: 1 MKSGLWYFLEFLCRLIKVLTG.....YMFMRVNTAKKSRLTDVTL 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 segs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	14.7	218	1	CD28_RAT
2	150.5	13.9	221	1	CD28_RABIT
3	141	13.0	219	1	CD28_BOVIN
4	139.5	12.9	220	1	CD28_HUMAN
5	138	12.8	218	1	CD28_MOUSE
6	97	9.0	221	1	CD28_CHICK
7	89	8.2	321	1	O5V1_HUMAN
8	87	8.0	330	1	FCG2_MOUSE
9	86.5	8.0	223	1	CTLA_MOUSE
10	86	7.9	223	1	CTLA_HUMAN
11	82.5	7.6	248	1	VGL2_EBV
12	81	7.5	1382	1	MET_RAT
13	81	7.5	1584	1	YJ9G_YEAST
14	77.5	7.2	324	1	CRFB_SHEEP
15	77.5	7.2	1070	1	PTK7_HUMAN
16	76.5	7.1	223	1	CTLA_RABIT
17	76.5	7.1	323	1	FCGC_HUMAN
18	76	7.0	317	1	FCGA_HUMAN
19	76	7.0	448	1	BCN1_MOUSE
20	76	7.0	450	1	BCN1_HUMAN
21	76	7.0	466	1	A1AA_RABIT
22	76	7.0	562	1	A1AD_MOUSE
23	75.5	7.0	261	1	FCG3_MOUSE
24	75	6.9	462	1	CATC_MOUSE
25	75	6.9	1132	1	VHST_LAMB
26	74.5	6.9	761	1	AD24_MOUSE
27	74	6.8	344	1	OM40_DROME
28	74	6.8	367	1	NUIM_PODAN
29	73.5	6.8	285	1	FCG2_RAT
30	73.5	6.8	322	1	CRFB_MOUSE
31	73.5	6.8	360	1	CCPH_HSVSA
32	73.5	6.8	496	1	GRB_MOUSE
33	73.5	6.8	496	1	GRB_RAT

34	73.5	6.8	497	1	GRB_HUMAN	P48167 homo sapien
35	73.5	6.8	1162	1	XBEN_CLOBU	Q06366 clostridium
36	73	6.7	275	1	YD84_YEAST	Q12359 saccharomyc
37	73	6.7	916	1	SCRB_LIMPO	Q25386 limulus pol
38	72.5	6.7	654	1	BFR2_HUMAN	Q01742 homo sapien
39	72	6.7	561	1	A1AD_RAT	P23944 rattus norv
40	72	6.7	569	1	YL53_YEAST	Q06567 saccharomyc
41	71.5	6.6	634	1	YCX3_EUGGR	P31916 euglena gra
42	71.5	6.6	1051	1	PTK7_CHICK	Q91048 gallus gall
43	71	6.6	212	1	KITH_ENCCU	Q96720 encephalitc
44	71	6.6	466	1	A1AA_BOVIN	P18130 bos taurus
45	70.5	6.5	524	1	VLI_HPV58	P26535 human papil

ALIGNMENTS

RESULT 1	ID	CD28_RAT	STANDARD	PRT	218 AA.
AC	P31042				
DT	01-JUL-1993 (Rel. 26, Created)				
DT	01-JUL-1993 (Rel. 26, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	T-cell-specific surface glycoprotein CD28 precursor.				
GN	CD28.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-DA; TISSUE-Lymphoid;				
RX	MEDLINE=92104640; PubMed=1309509;				
RA	Clark G.J., Dallman M.J.;				
RT	"Identification of a cDNA encoding the rat CD28 homologue.";				
RL	Immunogenetics 35:54-57(1992).				
CC	- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1				
CC	AND B7-2 (B70).				
CC	- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.				
CC	- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.				
CC	- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; X55288; CAA39003.1; -				
DR	PIR; S38722; S38722.				
DR	InterPro; IPR003600; Ig_Like.				
DR	SMART; SM00410; Ig_Like; 1.				
KW	Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.				
FT	SIGNAL 1				
FT	CHAIN 20				
FT	CD28.				
FT	EXTRACELLULAR (POTENTIAL).				
FT	POTENTIAL.				
FT	CYTOPLASMIC (POTENTIAL).				
FT	DOMAIN 151				
FT	DOMAIN 178				
FT	DOMAIN 29				
FT	CARBOHYD 72				
FT	CARBOHYD 93				
FT	CARBOHYD 106				
FT	CARBOHYD 130				
SO	SEQUENCE 218 AA; 25170 MW; 2E151C8F324C0B6E CRC64;				

Query Match 14.7%; Score 159; DB 1; Length 218;
Best Local Similarity 26.5%; Pred. NO. 2.1e-08;
Matches 41; Conservative 30; Mismatches 66; Indels 18; Gaps 7;

```

QY      30 MEFHNGVQLCKYPD--IVQQFKMOLKGGQILCDLTKTGSGNTVSIKSL-----F    82
       : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
Db      29 LVAVDNNEVLSCRYSYNNLAKEFRASLYKG--VNSDVEVCVGNGNETYPQFRPNVGFN   86
OY      83 CHSOLSNSVSFEFLYNLDHSHANYFCNLISIEDPPPE--KVTLTGGYLHTYESQLC---C    137
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
Db      87 CDGNEDNETVTETRLWNIDVNHDTDYECIEVMYPRPYLDNEKSNGTHIHLKEKHLCCHAQT   146
OY      138 QLEFWLPICCAAFVVNC-ILGCILIC-WLTKKK     168
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
Db      147 SKRLEWPLVVAVGVLLCYGLLVTVITLICIIWTNSRR   181

RESULT 2
CD28_RABIT STANDARD; PRT; 221 AA.
AC P42069;
01-NOV-1995 (Rel. 32, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
T-cell-specific surface glycoprotein CD28 precursor.
ORcytolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
[1] NCBI_TaxID=9986;
RN SEQUENCE FROM N.A.
RP STRAIN=B/J X CHB:H.M;
RX MEDLINE=95369849; PubMed=7642234;
RA Isono T., Seto A.;
RT "Cloning and sequencing of the rabbit gene encoding T-cell
costimulatory molecules.";
RL Immunogenetics 42:217-220(1995).
CC -! FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1
AND B7-2 (B70) (BY SIMILARITY).
CC -! SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -! CELLULAR LOCATION: Type I membrane protein.
CC -! SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -! SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outpost at
the European Bioinformatics institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/or
send an email to licenset@isb-sib.ch).
CC -----
DR EMBL; D49841; BAA08641.1; -.
DR InterPro; IPRO03600; IG_1like.
DR SMART; SM00410; IG_1like; 1.
KW Immunglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.
FT SIGNAL                      1          19
FT FT                          20         221
FT CHAIN                       20         221
FT                               CD28.
FT                                EXTRACELLULAR (POTENTIAL).
FT TRANSMEM                    151        177
FT FT                           178        221
FT DOMAIN                     29         138
FT FT                            38         38
FT CARBOHYD                   72         72
FT CARBOHYD                    93         93
FT CARBOHYD                   106        106
FT CARBOHYD                    130        130
FT SEQUENCE                  221 AA; 25307 MW; 3DF652C9CFCL4FI3 CRC64;

Query Match              13.9%; Score 150.5; DB 1; Length 221;
Best Local Similarity   23.8%; Pred. No. 1.4e-07;
Matches 38; Conservative 27; Mismatches 70; Indels 25; Gaps 6;
```

```

Db      29 MLYVNNNNEVNLSCKTYTNLFSEKFEERASLYKGADSAVEVCYVNGNFSPHQFHSHTGFn -- 86
Qy      81 KFCFSQLSNSVSFFLLYNLDHSHANYEFCNLISFDPPPF--KVTLTGYLHIYESQLC-- 136
Db      87 -CDGKLNETVFYLKNLVNQTDIYFCKIEVMYPPEYLDNEKSNGTIIHVKCEHCPCA 144
Qy      137 -----COLKFWLP|--GCCAFVVVCILGCILICWLTKR 168
Db      145 HPSBKSSTLFWVLVVGAVLAIFYSM LVVALFSCWMKSKR 184

RESULT 3
CD28_BOVIN
ID CD28_BOVIN STANDARD; PRT; 219 AA.
AC Q28071;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE T-cell-specific surface glycoprotein CD28 precursor.
GN CD28.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OX Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=96186531; PubMed=8606060;
RA Parsons K.R., Young J.R., Collins R.A., Howard C.J.;
RT "Cattle CTLA-4, CD28 and chicken CD28 bind CD86: MYPPPY is not
RT conserved in cattle CD28.";
RL Immunogenetics 43:388-391(1996).
CC -! FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1
CC AND B7-2 (B70).
CC -! SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -! SUBCELLULAR LOCATION: Type I membrane protein.
CC -! SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -! SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outpost at
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL; X93304; CAA63707.1; -.
CC InterPro; IPR003600; IG_Like.
DR SMART; SM00410; IG_Like; 1.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 FT POTENTIAL.
FT CHAIN 19 219 T-CELL-SPECIFIC SURFACE GLYCOPROTEIN
FT FT CD28.
FT DOMAIN 19 151 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 152 178 POTENTIAL.
FT DOMAIN 179 219 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 136 IG-LIKE V-TYPE DOMAIN.
FT CARBOHYD 37 37 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . . ) (POTENTIAL).
SQ SEQUENCE 219 AA; 25143 MW; 85B5C650E9634AA CRC64;

Query Match 13.0%; Score 141; DB 1; Length 219;
Best Local Similarity 23.2%; Pred. No. 1.2e-06;
Matches 36; Conservative 32; Mismatches 71; Indels 16; Gaps 6;

```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2002, 07:46:28 ; Search time 31 Seconds
(without alignments)
713.022 Million cell updates/sec

Title: US-09-823-307c-2
Perfect score: 1082
Sequence: 1 MKSGLWYFLLFLRLIKVLTG.....YMFMRVNTAKKSRLTDVTL 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802: *
1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT: *
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT: *
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT: *
4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT: *
5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT: *
6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT: *
7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT: *
8: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT: *
9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT: *
10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT: *
11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT: *
12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT: *
13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT: *
14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT: *
15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT: *
16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: *
17: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT: *
18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT: *
19: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT: *
20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *
21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT: *
22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1082	100.0	199	19 AAW75956	Human cell surface
2	1082	100.0	199	19 AAW75957	Human cell surface
3	1082	100.0	199	20 AAY08026	Human activated T-
4	1082	100.0	199	21 AAB08731	Amino acid sequenc
5	1082	100.0	199	22 AAE03428	Human gene 2 encod
6	1082	100.0	199	22 AAE03460	Human gene 2 encod
7	1082	100.0	199	22 AAE03525	Human secreted pro
8	1066.5	98.6	198	21 AAY92213	Human Th2-specific
9	737.5	68.2	200	21 AAY92212	Murine Th2-specific
10	734	67.8	200	21 AAB08723	Amino acid sequenc
11	722.5	66.8	200	19 AAW75958	Mouse cell surface

12	701	64.8	200	19 AAW71874	Rat cell surface p
13	696	64.3	216	19 AAW71875	Rat cell surface p
14	658	60.8	379	22 AAB67716	Amino acid sequenc
15	449.5	41.5	380	22 AAB67717	Amino acid sequenc
16	146.5	13.5	225	20 AAY41136	Rat CD28 protein s
17	145.5	13.4	221	21 AAY32286	Feline CD28. Feli
18	145.5	13.4	221	21 AAY32279	Cat CD28 receptor.
19	139.5	12.9	220	13 AAR20805	Human CD28 antigen
20	139.5	12.9	220	13 AAR27103	Sequence encoded b
21	139.5	12.9	220	17 AAW02131	Human CD28 cDNA pr
22	139.5	12.9	220	17 AAR91433	Human CD28 antigen
23	139.5	12.9	220	18 AAW38413	CD28. Homo sapien
24	139.5	12.9	220	19 AAW80442	Human CD28 antigen
25	139.5	12.9	220	20 AAW88451	Human CD28 antigen
26	139.5	12.9	220	21 AAY96128	Human cell surface
27	139.5	12.9	220	21 AAY44294	Human CD28 recepto
28	139.5	12.9	220	22 AAT02437	Human lymphocyte c
29	134	12.4	225	20 AAY41135	Mouse CD28 protein
30	126	11.6	223	20 AAY41137	Human CD28 protein
31	120.5	11.1	367	18 AAW35862	Human CD28: IgG2a c
32	119.5	11.0	134	18 AAW35846	Human CD28 for use
33	119.5	11.0	152	16 AAR67706	CD28 extracellular
34	89.5	8.3	117	20 AAY24469	Human CD28 gene pr
35	89	8.2	305	22 AAG66371	Human partial olfa
36	89	8.2	319	22 AAG71916	Human olfactory re
37	89	8.2	321	22 AAB46999	Human OLFXY protei
38	87.5	8.1	213	22 AAE04561	Human G-protein co
39	87	8.0	330	8 AAP70445	Sequence of mouse
40	86	7.9	223	18 AAW25111	Soluble human CTLA
41	86	7.9	223	22 AAG66519	Human CTLA4.. Homo
42	86	7.9	223	22 AAT00687	Human CTLA4 protei
43	85.5	7.9	187	19 AAW29728	Soluble CTLA4 muta
44	84.5	7.8	209	21 AAY94998	Human secreted pro
45	84	7.8	223	21 AAY15129	Human CTLA-4 prote

ALIGNMENTS

RESULT 1	
AAW75956	AAW75956 standard; Protein; 199 AA.
ID	AAW75956
XX	AAW75956;
AC	XX
XX	11-DEC-1998 (first entry)
DT	XX
XX	Human cell surface protein #1.
DE	XX
XX	Human; cell surface protein; thymocyte; lymphocyte; cell adhesion;
KW	signal transmission; autoimmune disorder; allergy; diagnosis;
KW	mitogen-stimulated.
OS	XX
OS	Homo sapiens.
XX	XX
XX	WO9838216-A1.
PN	XX
PD	03-SEP-1998.
XX	XX
PF	27-FEB-1998; 98WO-JP00837.
XX	XX
PR	26-FEB-1998; 98JP-0062217.
XX	27-FEB-1997; 97JP-0062290.
PA	(NISR) JAPAN TOBACCO INC.
XX	XX
PI	Tamatani T, Teruka K;
XX	XX
DR	WPI; 1998-48144/41.
DR	N-PSDB; AAV53198.
XX	XX
PT	Cell surface molecule expressed in thymocytes and lymphocytes and - mediating signal transmission and cell adhesion, and antibodies to

PT It useful in treatment of autoimmune and allergic disorders.
XX
PS Claim 2; Page 99-101; 149pp; Japanese.
XX
CC The present sequence represents a human cell surface protein which is
CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
CC antibodies recognising the cell surface protein. These antibodies also
CC produce an increase in peripheral blood lymphocytes in the presence of
CC an antibody recognising CD3 antigen. The cell surface protein contains
CC the amino acid sequence FDPDPF in its extracellular region and the
CC sequence YMF in its intracellular region. The cell surface protein can
CC be used in the prevention and treatment of autoimmune and allergic
CC diseases, and in the diagnosis and investigation of such disorders.
XX
SQ Sequence 199 AA;

Query Match 100.0%; Score 1082; DB 19; Length 199;
Best Local Similarity 100.0%; Pred. No. 6.6e-116;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 M K S G L W Y F F L F C L R I K V L T G E I N G S A N Y E M F I F H N G V Q I L C K Y P D I V Q O F K M Q L L K G Q 60
Db 1 M K S G L W Y F F L F C L R I K V L T G E I N G S A N Y E M F I F H N G V Q I L C K Y P D I V Q O F K M Q L L K G Q 60

OY 61 I L C D L T K T K G S G N T V S I K S L K F C H S Q L S N N S V S F F L Y N L D H S H A N Y F C N L S I F D P P P F K 120
Db 61 I L C D L T K T K G S G N T V S I K S L K F C H S Q L S N N S V S F F L Y N L D H S H A N Y F C N L S I F D P P P F K 120

OY 121 V T L T G Y L H I Y E S Q L C C Q L K F W L P I G C A F V V V C I L G C I L C W L T K K K Y S S V H D P N G E Y 180
Db 121 V T L T G Y L H I Y E S Q L C C Q L K F W L P I G C A F V V V C I L G C I L C W L T K K K Y S S V H D P N G E Y 180

OY 181 M F M R A V N T A K K S R L T D V T L 199
Db 181 M F M R A V N T A K K S R L T D V T L 199

RESULT 2
AAW75957
ID AAW75957 standard; Protein; 199 AA.
XX
AC AAW75957;
XX
DT 11-DEC-1998 (first entry)
XX
DE Human cell surface protein #2.
XX
KW Human; cell surface protein; thymocyte; lymphocyte; cell adhesion;
KW signal transmission; autoimmune disorder; allergy; diagnosis;
KW mitogen-stimulated.
XX
OS Homo sapiens.
XX
PN WO9838216-A1.
XX
PD 03-SEP-1998.
XX
PF 27-FEB-1998; 98WO-JP00837.
XX
PR 26-FEB-1998; 98JP-0062217.
PR 27-FEB-1997; 97JP-0062290.
XX
PA (NISR) JAPAN TOBACCO INC.
XX
PI Tamatani T, Tezuka K;
XX
DR WPI; 1998-481144/41.
DR N-PSDB; AAV53199.
XX
PT Cell surface molecule expressed in thymocytes and lymphocytes and
PT mediating signal transmission and cell adhesion, and antibodies to
PT it useful in treatment of autoimmune and allergic disorders.
XX

XX
PS Claim 9; Page 101-105; 149pp; Japanese.
XX
CC The present sequence represents a human cell surface protein which is
CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
CC antibodies recognising the cell surface protein. These antibodies also
CC produce an increase in peripheral blood lymphocytes in the presence of
CC an antibody recognising CD3 antigen. The cell surface protein contains
CC the amino acid sequence FDPDPF in its extracellular region and the
CC sequence YMF in its intracellular region. The cell surface protein can
CC be used in the prevention and treatment of autoimmune and allergic
CC diseases, and in the diagnosis and investigation of such disorders.
XX
SQ Sequence 199 AA;

Query Match 100.0%; Score 1082; DB 19; Length 199;
Best Local Similarity 100.0%; Pred. No. 6.6e-116;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 M K S G L W Y F F L F C L R I K V L T G E I N G S A N Y E M F I F H N G V Q I L C K Y P D I V Q O F K M Q L L K G Q 60
Db 1 M K S G L W Y F F L F C L R I K V L T G E I N G S A N Y E M F I F H N G V Q I L C K Y P D I V Q O F K M Q L L K G Q 60

OY 61 I L C D L T K T K G S G N T V S I K S L K F C H S Q L S N N S V S F F L Y N L D H S H A N Y F C N L S I F D P P P F K 120
Db 61 I L C D L T K T K G S G N T V S I K S L K F C H S Q L S N N S V S F F L Y N L D H S H A N Y F C N L S I F D P P P F K 120

OY 121 V T L T G Y L H I Y E S Q L C C Q L K F W L P I G C A F V V V C I L G C I L C W L T K K K Y S S V H D P N G E Y 180
Db 121 V T L T G Y L H I Y E S Q L C C Q L K F W L P I G C A F V V V C I L G C I L C W L T K K K Y S S V H D P N G E Y 180

OY 181 M F M R A V N T A K K S R L T D V T L 199
Db 181 M F M R A V N T A K K S R L T D V T L 199

RESULT 3
AAY08026
ID AAY08026 standard; Protein; 199 AA.
XX
AC AAY08026;
XX
DT 08-JUL-1999 (first entry)
XX
DE Human activated T-lymphocyte protein 8F4.
XX
KW T-lymphocyte; human; 8F4; T cell co-stimulation; activated; CD4+; CD8+;
KW anticancer; antiviral; anti-asthma; immunomodulator; proliferation;
KW T cell activation; cytokine synthesis; regulatory element; B cell;
KW T cell-dependent antibody production; treatment; prevention; cancer;
KW autoimmune disease; transplant rejection; immune system regulation;
KW disorder; acquired immune deficiency syndrome; AIDS; asthma.
XX
OS Homo sapiens.
XX
PN WO9915553-A2.
XX
PD 01-APR-1999.
XX
PF 23-SEP-1998; 98WO-DE02896.
XX
PR 11-MAY-1998; 98DE-1021060.
PR 23-SEP-1997; 97DE-1041929.
XX
PA (DEKO-) DEUT KOCH INST ROBERT.
PA (BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.
XX
PI Kroczeck R;
XX
DR WPI; 1999-276975/23.
DR N-PSDB; AAX37661.
XX

PT Polypeptide 8F4 co-stimulates T cells and is present only on
PT activated cells
XX
PS Claim 2; Page 24; 47pp; German.
CC This invention describes a novel human protein, 8F4, and its encoding
CC nucleic acid which co-stimulates T cells and is present on activated CD4+
CC and CD8+ T cells but not on resting or activated B cells, granulocytes,
CC monocytes, natural killer or dendritic cells. 8F4 has anticancer,
CC antiviral, anti-asthma and immunomodulatory activity. 8F4 provides a
CC strong co-stimulatory signal for T cell activation, i.e. it amplifies
CC proliferation of T cells, synthesis of certain cytokines and other
CC regulatory agents, and improves T cell-dependent antibody production
CC by B cells. Agents that inhibit 8F4 are used to treat or prevent
CC autoimmune diseases, to prevent transplant rejection and to treat
CC disorders of immune system regulation. 8F4, or cells that express it,
CC is/are used to treat or prevent cancers, acquired immune deficiency
CC syndrome, asthma and chronic infectious diseases (e.g. hepatitis B or C).
XX
SQ Sequence 199 AA;
Y Match 100.0%; Score 1082; DB 20; Length 199;
Best Local Similarity 100.0%; Pred. No. 6.6e-116;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKSGLMWFFFLCLRIKVLTEINGSANYEMFIFHNGVQILCKYPDIYQQFKMQLKGGQ 60
1 MKSGLMWFFFLCLRIKVLTEINGSANYEMFIFHNGVQILCKYPDIYQQFKMQLKGGQ 60
Db 1 MKSGLMWFFFLCLRIKVLTEINGSANYEMFIFHNGVQILCKYPDIYQQFKMQLKGGQ 60
QY 61 ILCDLTKTKGSGNTVSIRKSLKFCCHSOLSNNSVSFFLYNLDSHANYFCNLSIFDPPPFK 120
61 ILCDLTKTKGSGNTVSIRKSLKFCCHSOLSNNSVSFFLYNLDSHANYFCNLSIFDPPPFK 120
Db 61 ILCDLTKTKGSGNTVSIRKSLKFCCHSOLSNNSVSFFLYNLDSHANYFCNLSIFDPPPFK 120
QY 121 VTLTGGYLHIYESQLCCQKFWLPIGCAAFVVCILGICILICWLTKKKYSSSVHDPNGEY 180
121 VTLTGGYLHIYESQLCCQKFWLPIGCAAFVVCILGICILICWLTKKKYSSSVHDPNGEY 180
Db 121 VTLTGGYLHIYESQLCCQKFWLPIGCAAFVVCILGICILICWLTKKKYSSSVHDPNGEY 180
QY 181 MFMRAVNTAKKSRLTDVTL 199
181 MFMRAVNTAKKSRLTDVTL 199
Db 181 MFMRAVNTAKKSRLTDVTL 199
RESULT 4
AAB08731
ID AAB08731 standard; Protein; 199 AA.
XX
AC AAB08731;
XX
XX 02-JAN-2001 (first entry)
X Amino acid sequence of a human CRP1 polypeptide.
DL
XX
KW CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;
KW T-lymphocyte activation; type I transmembrane protein; T cell activation;
KW T cell proliferation; T-cell mediated disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note= "signal peptide"
FT Protein 21..199
FT /note= "mature protein"
FT Domain 21..140
FT /note= "extracellular domain"
FT Domain 141..161
FT /note= "predicted transmembrane domain"
FT Domain 162..199
FT /note= "intracellular domain"
XX
PN WO2000046240-A2.
XX
PD 10-AUG-2000.

XX
PF 27-JAN-2000; 2000WO-US01871.
XX
PR 03-FEB-1999; 99US-0244448.
PR 08-MAR-1999; 99US-0264527.
XX
PA (AMGE-) AMGEN INC.
XX
PI Yoshinaga SK;
XX
DR WPI; 2000-543476/49.
DR N-PSDB; AAA64558.
XX
PT Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
PT in the treatment, prevention and diagnosis of T cell mediated disorders
XX
PS Disclosure; Fig 13A; 174pp; English.
XX
CC The present sequence represents a CRP1 (CD28 related protein-1)
CC polypeptide. The specification also describes a B7RP1 (B7 related
CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
CC activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
CC predicted to be a type I transmembrane protein. The nucleic acids are
CC useful for regulating T cell activation or proliferation in an animal.
CC The polypeptides are useful for treating, preventing ameliorating or
CC diagnosing a T-cell mediated disorder in an animal. They can also be
CC used to identify test molecules that bind to the polypeptides.
XX
SQ Sequence 199 AA;
Query Match 100.0%; Score 1082; DB 21; Length 199;
Best Local Similarity 100.0%; Pred. No. 6.6e-116;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKSGLMWFFFLCLRIKVLTEINGSANYEMFIFHNGVQILCKYPDIYQQFKMQLKGGQ 60
1 MKSGLMWFFFLCLRIKVLTEINGSANYEMFIFHNGVQILCKYPDIYQQFKMQLKGGQ 60
Db 1 MKSGLMWFFFLCLRIKVLTEINGSANYEMFIFHNGVQILCKYPDIYQQFKMQLKGGQ 60
QY 61 ILCDLTKTKGSGNTVSIRKSLKFCCHSOLSNNSVSFFLYNLDSHANYFCNLSIFDPPPFK 120
61 ILCDLTKTKGSGNTVSIRKSLKFCCHSOLSNNSVSFFLYNLDSHANYFCNLSIFDPPPFK 120
Db 61 ILCDLTKTKGSGNTVSIRKSLKFCCHSOLSNNSVSFFLYNLDSHANYFCNLSIFDPPPFK 120
QY 121 VTLTGGYLHIYESQLCCQKFWLPIGCAAFVVCILGICILICWLTKKKYSSSVHDPNGEY 180
121 VTLTGGYLHIYESQLCCQKFWLPIGCAAFVVCILGICILICWLTKKKYSSSVHDPNGEY 180
Db 121 VTLTGGYLHIYESQLCCQKFWLPIGCAAFVVCILGICILICWLTKKKYSSSVHDPNGEY 180
QY 181 MFMRAVNTAKKSRLTDVTL 199
181 MFMRAVNTAKKSRLTDVTL 199
Db 181 MFMRAVNTAKKSRLTDVTL 199
RESULT 5
AAE03428
ID AAE03428 standard; Protein; 199 AA.
XX
AC AAE03428;
XX
DT 10-AUG-2001 (first entry)
DE Human gene 2 encoded secreted protein HT2SG64, SEQ ID NO: 111.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
KW inflammation; neurological disorder; Alzheimer's disease; food additive;
KW angiotensin disorder; kidney disorder; gastrointestinal disorder; allergy;
KW pregnancy-related disorder; endocrine disorder; infection; wound healing;
KW cell culture; chemotaxis; vulnery; binding partner identification;
KW gene therapy.
XX


```
OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= Signal_peptide
FT Protein 20..111
FT /note= "Mature human secreted protein"
XX
XX WO200132675-A1.
XX PD 10-MAY-2001.
XX
XX PF 25-OCT-2000; 2000WO-US29363.
XX
XX PR 29-OCT-1999; 99US-0162239.
XX PR 30-JUN-2000; 2000US-0215139.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Komatsoulis GA, Wei P, Baker KP, Young PE;
XX WPI; 2001-328772/34.
XX N-PSDB; AAD07810.
XX
XX Claim 11: Page 471; 576pp; English.
XX
XX AAD07809-AAD07907 represent cDNAs corresponding to 32 human secreted
XX protein genes, and AAE03427-AAE03523 represent the proteins they encode.
XX AAE03524-AAE03537 represent human secreted protein fragments or variants.
XX The secreted proteins and their genes are useful for preventing, treating
XX or ameliorating medical conditions, e.g., by protein or gene therapy.
XX Pathological conditions can be diagnosed by determining the amount of the
XX new protein in a sample or by determining the presence of mutations in
XX the new genes. Specific uses are described for each of the 32 genes,
XX based on the tissues in which they are most highly expressed, and include
XX developing products for the diagnosis or treatment of proliferative
XX disorders, cancer, tumours, foetal and developmental abnormalities,
XX haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
XX diseases (e.g., rheumatoid arthritis), inflammation, allergies,
XX neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
XX cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
XX psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
XX angiotensin disorders, kidney disorders, gastrointestinal disorders,
XX pregnancy-related disorders, endocrine disorders, and infections. The
XX proteins can also be used to aid wound healing and epithelial cell
XX proliferation, to prevent skin aging due to sunburn, to maintain organs
XX before transplantation, for supporting cell culture of primary tissues,
XX to regenerate tissues, to identify their cognate ligands or binding
XX partners, and in chemotaxis, and can be used as a food additive or a
XX preservative to modify storage properties. Antibodies specific for a
XX protein of the invention can be used in alleviating symptoms associated
XX with the disorders mentioned above, and in diagnostic immunoassays e.g.,
XX radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
XX The present sequence represents a human secreted protein of
XX the invention.
XX
XX SQ Sequence 199 AA:
XX
XX Query Match 100.0%; Score 1082; DB 22; Length 199;
XX Best Local Similarity 100.0%; Pred. No. 6.6e-116;
XX Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MKSGLMWFFLFCRLRIKVLTEINGSANYEMFIHNGVQILCKYPDIVQEFKMQMLKGGQ 60
XX |||||||
XX DB 1 MKSGLMWFFLFCRLRIKVLTEINGSANYEMFIHNGVQILCKYPDIVQEFKMQMLKGGQ 60
XX
XX QY 61 ILCDLTKTKGSGNTVSIKSLKFCCHSOLSNNSVSFFLYNLDSHANYFCNLSIFDPPPPK 120
XX |||||||
XX DB 61 ILCDJTKTKGSGNTVSIKSLKFCCHSOLSNNSVSFFLYNLDSHANYFCNLSIFDPPPPK 120
```

```
QY 121 VTLTGGLHIIYESQLCCQLKFWLPICGAFVWVCILGCLICMLTKKKYSSVHPDNGEY 180
XX |||||||
DB 121 VTLTGGLHIIYESQLCCQLKFWLPICGAFVWVCILGCLICMLTKKKYSSVHPDNGEY 180
QY 181 MEMRAVNTAKRSRLTDVTL 199
XX |||||||
DB 181 MEMRAVNTAKRSRLTDVTL 199
XX
XX RESULT 6
XX AAE03460
XX ID AAE03460 standard; Protein; 199 AA.
XX
XX AC AAE03460;
XX
XX DT 10-AUG-2001 (first entry)
XX
XX DE Human gene 2 encoded secreted protein HT2SG64, SEQ ID NO: 143.
XX
XX XX Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
XX foetal abnormality; developmental abnormality; haematopoietic disorder;
XX immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
XX Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
XX psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
XX inflammation; neurological disorder; Alzheimer's disease; food additive;
XX angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy;
XX pregnancy-related disorder; endocrine disorder; infection; wound healing;
XX cell culture; chemotaxis; vulnerability; binding partner identification;
XX gene therapy.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..19
XX FT /label= Signal_peptide
XX FT Protein 20..199
XX FT /note= "Mature human secreted protein"
XX
XX WO200132675-A1.
XX
XX PD 10-MAY-2001.
XX
XX PF 25-OCT-2000; 2000WO-US29363.
XX
XX PR 29-OCT-1999; 99US-0162239.
XX PR 30-JUN-2000; 2000US-0215139.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Komatsoulis GA, Wei P, Baker KP, Young PE;
XX WPI; 2001-328772/34.
XX N-PSDB; AAD07842.
XX
XX Claim 11: Page 489-490; 576pp; English.
XX
XX AAD07809-AAD07907 represent cDNAs corresponding to 32 human secreted
XX protein genes, and AAE03427-AAE03523 represent the proteins they encode.
XX AAE03524-AAE03537 represent human secreted protein fragments or variants.
XX The secreted proteins and their genes are useful for preventing, treating
XX or ameliorating medical conditions, e.g., by protein or gene therapy.
XX Pathological conditions can be diagnosed by determining the amount of the
XX new protein in a sample or by determining the presence of mutations in
XX the new genes. Specific uses are described for each of the 32 genes,
XX based on the tissues in which they are most highly expressed, and include
XX developing products for the diagnosis or treatment of proliferative
XX disorders, cancer, tumours, foetal and developmental abnormalities,
XX haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
```

diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein of the invention.

SQ Sequence 199 AA;

ty Match	100.0%;	Score 1082;	DB 22;	Length 199;
: Local Similarity	100.0%;	Pred. No. 6.6e-116;		
Matches 199;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MKSGLMWFEFLECLRIKAVLTGEINGSANYEMFIHNGGVQILCKXPDIVOQFKMQLLKGGQ	60
Dd	1	MKSGLMWFLEFLCRLIKVLTGEINGSANYEMEIFHNGGVQILCKXPDIVOQFKMQLLKGGQ	60
QY	61	ILCDLTKTKGSGNTVSIKSLKECHSOLSNNNSVSSEFLYNLDHSHANYEFCNLSIFDPPPFK	120
Dd	61	ILCDLTKTKKGSGNTVSIKSLKECHSOLSNNNSVSSEFLYNLDHSHANYEFCNLSIFDPPPFK	120
QY	121	VTLTGXYLHIYESQOLCCQKLFWLPICGAFFVVCILGCILICWLTKKKKYSSSVHDPNGEY	180
Dd	121	VTLTGXYLHIYESQOLCCQKLFWLPICGAFFVVCILGCILICWLTKKKKYSSSVHDPNGEY	180
QY	181	MEMRAVNATAKKSRLTDVTL 199	
Dd	181	MEMRAVNATAKKSRLTDVTL 199	

RESULT 7

ID	AAE03525	standard; Protein; 199 AA.
----	----------	----------------------------

AC AAE03525

DT 10-AUG-2001 (first entry)

Human secreted protein variant, SEQ ID NO: 211.

Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; alzheimer's disease; food additive; angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnery; binding partner identification; gene therapy.

..... Homo sapiens.

PN W0200132675-A1.

PD 10-MAY-2001.

25-OCT-2000; 2000WO-US29363

29-OCT-1999: 99US-0162239

30-JUN-2000; 200005-0215159
PK
XX

XX

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Komatsoulis GA, Wei P, Baker KP, Young PE;

DR WPI; 2001-328772/34

PT Thirty two human secreted proteins, useful for treating cancers, hyperproliferative disorders, inflammatory disorders, neurological disorders, autoimmune diseases and cardiovascular disorders -

PS Disclosure; Page 524; 576pp; English.

CC AAD07809 AAD07907 represent cDNAs corresponding to 32 human secreted
CC protein genes, and AAE03427-AAE03523 represent the proteins they encode.
CC AAE03524-AAE03537 represent human secreted protein fragments or variants.
CC The secreted proteins and their genes are useful for preventing, treating
CC or ameliorating medical conditions, e.g., by protein or gene therapy.
CC Pathological conditions can be diagnosed by determining the amount of the
CC new protein in a sample or by determining the presence of mutations in
CC the new genes. Specific uses are described for each of the 32 genes,
CC based on the tissues in which they are most highly expressed, and include
CC developing products for the diagnosis or treatment of proliferative
CC disorders, cancer, tumours, foetal and developmental abnormalities,
CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
CC pregnancy-related disorders, endocrine disorders, and infections. The
CC proteins can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues, to identify their cognate ligands or binding
CC partners, and in chemotaxis, and can be used as a food additive or
CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
CC The present sequence represents a human secreted protein variant
CC referred to in the disclosure of the invention.

Sequence 199 AA;

Query Match	100.0%;	Score 1082;	DB 22;	Length 199;
Best Local Similarity	100.0%;	Pred. No. 6.6e-116;		
Matches 199;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MKSGLMWFFLLFCRLRIKVLVTGEINGSANYEMFIHNGGVQLCKYPDIVOQFKMQLLKGGQ	60
Dd	1	MKSGLMWFFLLFCRLRIKVLVTGEINGSANYEMFIHNGGVQLCKYPDIVOQFKMQLLKGGQ	60
QY	61	IILCDLTKTGSGSNTVSIRKSLKEFCHSQLSNNNSVSEFLYNIDHSNANYFYFCNL.SIFDPPEPK	120C
Dd	61	IILCDLTKTGSGSNTVSIRKSLKEFCHSQLSNNNSVSEFLYNIDHSNANYFYFCNL.SIFDPPEPK	120C
QY	121	VTLTGGYLHIYESOLCCOLKEFWLPICGCAAFVVVCILGCITLCWLTKKKYSSSVHDPNGEY	180C
Dd	121	VTLTGGYLHIYESOLCCOLKEFWLPICGCAAFVVVCILGCITLCWLTKKKYSSSVHDPNGEY	180C
QY	181	MEMRAVNTAKKSRLTDVTL	199
b	181	MEMRAVNTAKKSRLTDVTL	199

RESULT 8

ID AAY92213 standard; Protein; 198 AA.

AC AAY92213;

DT 10-AUG-2000 (first entry)

XX 5

```
DE Human Th2-specific polypeptide, h1228.
XX
XX h1228; Th2-specific; T helper cell; anti-inflammatory; antiarthritic;
KW CD28; antidiabetic; immunosuppressive; neuroprotective; dermatological;
KW antipsoriatic; antiasthmatic; antiallergic; anti-viral; ophthalmological;
KW CTLA-4; nephroretropic; anti-HIV; antibacterial.
XX
OS Homo sapiens.
XX
FH Key .Location/Qualifiers
FT Peptide 113..118
FT /label= conserved_PPP_motif
FT /note= "common in CD28 and CTLA-4"
FT
FT Peptide 178..181
FT /label= YXXM_motif
FT /note= "common in CD28 and CTLA-4; necessary for
FT CD28-mediated phosphatidylinositol 3-kinase
FT activity"
FT
XX WO200019988-A1.
XX 13-APR-2000.
XX
XX 06-OCT-1999; 99WO-US23156.
XX PF
XX 07-OCT-1998; 98US-0168229.
XX PR
XX 26-FEB-1999; 99US-0258670.
XX PR
XX 06-OCT-1999; 99US-0413136.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Lehar S, Manning S, Coyle AJ, Gutierrez-ramos J;
XX WPI; 2000-303619/26.
XX DR
XX N-PSDB; AAA09056.
XX
XX T helper (Th) 2 nucleic acids and encoded proteins, useful for the
XX diagnosis and treatment of immune and respiratory disorders such as
XX Crohn's diseases, arthritis, insulin dependent diabetes and
XX autoimmunity
XX
XX Claim 16; Page 138-139; 159pp; English.
XX
XX This Th2-specific polypeptide, which has similarity to human CD28 and
XX human CTLA-4 is encoded by human orthologue h1228.
XX A novel method for modulating a Th2 response, an immune response, or
XX suppressing airway inflammation or hyperresponsiveness in a mammal
XX comprises administering a Th2-specific polypeptide of the invention, an
XX antibody to such a polypeptide or allelic variants of the genes. The
XX novel DNA and polypeptide sequences are useful for treatment and
XX diagnosis of Th cell and Th cell-like disorders such as Crohn's diseases,
XX arthritis, insulin dependent diabetes, autoimmunity, multiple sclerosis,
XX dermatitis, psoriasis, graft rejection, graft versus host diseases,
XX sarcoidosis, asthma, allergies, conjunctivitis, glomerular nephritis,
XX viral infections (including human immunodeficiency virus (HIV)),
XX bacterial infections, bronchitis, cystic fibrosis, diptheria,
XX emphysema, pneumonia, and Legionnaires disease.
XX
XX Sequence 198 AA;
SQ
Query Match 98.6%; Score 1066.5; DB 21; Length 198;
Best Local Similarity 99.5%; Pred. No. 3.9e-114;
Matches 198; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
DB 121 VTLTGGLHYESQLCCQLKFWLPICGAFVVCILGICILCWLTKKKYSSVHDPNGEY 179
QY 181 MFMRAVNTAKKSRLTDVTL 199
DB 180 MFMRAVNTAKKSRLTDVTL 198

RESULT 9
AAAY92212
ID AAY92212 standard; Protein; 200 AA.
XX
XX AAY92212;
AC
XX 10-AUG-2000 (first entry)
DF
XX
XX Murine Th2-specific polypeptide, m1228.
DE
XX
XX m1288; Th2-specific; T helper cell; anti-inflammatory; antiarthritic;
KW CD28; antidiabetic; immunosuppressive; neuroprotective; dermatological;
KW antipsoriatic; antiasthmatic; antiallergic; anti-viral; ophthalmological;
KW CTLA-4; nephroretropic; anti-HIV; antibacterial.
XX
XX Mus musculus.
OS
XX
XX Key .Location/Qualifiers
XX FH 114..119
XX FT /label= conserved_PPP_motif
XX FT /note= "common in CD28 and CTLA-4"
XX FT
XX FT Peptide 181..184
XX FT /label= YXXM_motif
XX FT /note= "common in CD28 and CTLA-4; necessary for
XX CD28-mediated phosphatidylinositol 3-kinase
XX activity"
XX
XX WO200019988-A1.
XX 13-APR-2000.
XX
XX 06-OCT-1999; 99WO-US23156.
XX PF
XX 07-OCT-1998; 98US-0168229.
XX PR
XX 26-FEB-1999; 99US-0258670.
XX PR
XX 06-OCT-1999; 99US-0413136.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Lehar S, Manning S, Coyle AJ, Gutierrez-ramos J;
XX WPI; 2000-303619/26.
XX DR
XX N-PSDB; AAA09054.
XX
XX T helper (Th) 2 nucleic acids and encoded proteins, useful for the
XX diagnosis and treatment of immune and respiratory disorders such as
XX Crohn's diseases, arthritis, insulin dependent diabetes and
XX autoimmunity
XX
XX Claim 16; Page 130-131; 159pp; English.
XX
XX This Th2-specific polypeptide is encoded by a murine orthologue m1288.
XX The protein shares homology with both human and murine CD28 and CTLA-4.
XX A novel method for modulating a Th2 response, an immune response, or
XX suppressing airway inflammation or hyperresponsiveness in a mammal
XX comprises administering a Th2-specific polypeptide of the invention, an
XX antibody to such a polypeptide or allelic variants of the genes. The
XX novel DNA and polypeptide sequences are useful for treatment and
XX diagnosis of Th cell and Th cell-like disorders such as Crohn's diseases,
XX arthritis, insulin dependent diabetes, autoimmunity, multiple sclerosis,
XX dermatitis, psoriasis, graft rejection, graft versus host diseases,
XX sarcoidosis, asthma, allergies, conjunctivitis, glomerular nephritis,
XX viral infections (including human immunodeficiency virus (HIV)),
XX bacterial infections, bronchitis, cystic fibrosis, diptheria,
XX emphysema, pneumonia, and Legionnaires disease.
XX
```

```

XX      Sequence      200 AA:
SQ
Query Match
Best Local Similarity 68.2%; Score 737.5; DB 21; Length 200;
Matches 138; Conservative 20; Mismatches 40; Indels 1; Gaps 1;
QY      1 M K S G L W F E F L C L R I K V L T G E I N G S A N Y E M F I F H N G V Q I L C K Y P D I V Q Q F K M Q L K G G Q 60
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      1 M K P Y F C H V F E F C F L I R L L T G E I N G S A D H R M E S F H N G V Q I S C K Y P E T V Q Q L K M R L F R E R E 60
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      61 I L C D L T K T K G S G N T V S I K S L K F C H S Q L S N N S V S F F L Y N L D H S H A N Y Y E C N L S I F D P P P F K 120
      61 V L C E L T K T K G S G N A V S I K N P M L C L Y H L S N N S V S F F L N P D S S Q G S Y Y F C S L S I F D P P P F Q 120
QY      121 V - T L T G G Y L H I Y E S Q L C C Q L K F W L P I G C A F V V V C I L G C I L C W L T K K Y S S V H D P N G E 179
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      121 E R N L S G Y L H I Y E S Q L C C Q L K W L P V G C A F V V V L L F G C I L I I W F S K K K Y G S S V H D P N S E 180
QY      180 Y M F M R A V N T A K K S R L T D V T 198
      111 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      181 Y M F M A A V N T N K K S R L A G V T 199
DI
RESULT 10
AAB08723
ID      AAB08723 standard; Protein; 200 AA.
XX      AAB08723;
AC
XX      02-JAN-2001 (first entry)
DT
XX      Amino acid sequence of a murine CRP1 polypeptide.
DE
XX
KW      CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;
KW      T-lymphocyte activation; type I transmembrane protein; T cell activation;
KW      T cell proliferation; T-cell mediated disorder.
XX
OS      Mus sp.
XX
FH      Key Location/Qualifiers
FT      Peptide 1..20
FT      Protein /note= "signal peptide"
FT      Protein 21..200
FT      Domain /note= "mature protein"
FT      Domain /note= "extracellular domain"
FT      Domain 146..163
FT      Domain /note= "predicted transmembrane domain"
FT      Domain 164..200
FT      Domain /note= "intracellular domain"
PN      WO200046240-A2.
XX
PD      10-AUG-2000.
XX
PF      27-JAN-2000; 2000WO-US01871.
XX
PR      03-FEB-1999; 99US-0244448.
PR      08-MAR-1999; 99US-0264527.
XX
PA      (AMGE-) AMGEN INC.
XX
PI      Yoshinaga SK;
XX
DR      WPI; 2000-543476/49.
DR      N-PSDB; AAA64554.
XX
PT      Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
PT      in the treatment, prevention and diagnosis of T cell mediated disorders
XX
PS      Claim 11; Fig 1A; 174pp; English.
```

```

XX      The present sequence represents a CRP1 (CD28 related protein-1)
CC      polypeptide. The specification also describes a B7RP1 (B7 related
CC      protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
CC      activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
CC      predicted to be a type I transmembrane protein. The nucleic acids are
CC      useful for regulating T cell activation or proliferation in an animal.
CC      The polypeptides are useful for treating, preventing ameliorating or
CC      diagnosing a T-cell mediated disorder in an animal. They can also be
CC      used to identify test molecules that bind to the polypeptides.
XX
SQ      Sequence      200 AA:
QY      7 Y F - - - F L F C L R I K V L T G E I N G S A N Y E M F I F H N G V Q I L C K Y P D I V Q Q F K M Q L K G G Q I L C 63
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      4 Y F C R V F E F C F L I R L L T G E I N G S A D H R M E S F H N G V Q I S C K Y P E T V Q Q L K M R L F R E R E Y I L C 63
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      64 D L T K T K G S G N T V S I K S L K F C H S Q L S N N S V S F F L Y N L D H S H A N Y Y E C N L S I F D P P P F K Y - T 122
      64 E L T K T K G S G N A V S I K N P M L C L Y H L S N N S V S F F L N P D S S Q G S Y Y F C S L S I F D P P P F Q E R N 123
QY      123 L T G G Y L H I Y E S Q L C C Q L K F W L P I G C A F V V V C I L G C I L C W L T K K Y S S V H D P N G E Y M F 182
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      124 L S G G Y L H I Y E S Q L C C Q L K W L P V G C A F V V V L L F G C I L I I W F S K K K Y G S S V H D P N S E Y M F 183
QY      183 M R A V N T A K K S R L T D V T 198
      111 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      184 M A A V N T N K K S R L A G V T 199
DB
AAW75958
ID      AAW75958 standard; Protein; 200 AA.
XX      AAW75958;
AC
XX      11-DEC-1998 (first entry)
DT
XX      Mouse cell surface protein.
DE
XX
KW      Mouse; cell surface protein; thymocyte; lymphocyte; cell adhesion;
KW      signal transduction; autoimmune disorder; allergy; diagnosis;
KW      mitogen-stimulated.
XX
OS      Mus sp.
XX
PN      WO9838216-A1.
XX
PD      03-SEP-1998.
XX
PF      27-FEB-1998; 98WO-JP00837.
XX
PR      26-FEB-1998; 98JP-0062217.
PR      27-FEB-1997; 97JP-0062290.
XX
PA      (NISB ) JAPAN TOBACCO INC.
XX
PI      Tamatani T, Tezuka K;
XX
DR      WPI; 1998-481144/41.
DR      N-PSDB; AAV53200.
XX
PT      Cell surface molecule expressed in thymocytes and lymphocytes and
PT      mediating signal transduction and cell adhesion, and antibodies to
PT      it useful in treatment of auto-immune and allergic disorders.
XX
PS      Claim 9; Page 110-112; 149pp; Japanese.
XX
CC      The present sequence represents a mouse cell surface protein which is
```


CC response in a subject. GL50 polypeptides are used to modulate T cell
CC costimulation, and to reduce the proliferation of a tumour cell. Diseases
CC that can be treated using GL50 molecules are graft-versus-host disease,
CC autoimmune disease, allergies, acquired immune deficiency syndrome
CC (AIDS), and viral infections. The GL50 molecules can be used in vaccines.
CC GL50 polynucleotides can be used to locate gene regions associated with
CC genetic disease, in tissue typing, and in forensic identification of a
CC biological sample.

XX
SQ Sequence 380 AA;

Query Match 41.5%; Score 449.5; DB 22; Length 380;
Best Local Similarity 70.2%; Pred. No. 6.5e-43;
Matches 85; Conservative 13; Mismatches 22; Indels 1; Gaps 1;

QY 21 EINGSAN YEMFIHNGGVQILCKYPDIVQPFKQQLKGGQILCDLTKTKSGSGNTVSISL 80
| | | | | : | | | | | | | | | | : | | : | | : | | | | | | | | | |
Db 26 EINGSADHRMFSFHNGGVQISCKYPETVQQLKRLFREREVLCELTKTKSGGNVSIKNP 85
| | | | | : | | | | | | | | | | : | | : | | : | | | | | | | | | |
81 KFCHS QLSNNSVSFFLYNLDSHANYFCNLSIFDPPPFKV-TLTGGLHIYESQLCCQL 139
| | | | | : | | | | | | | | | | : | | : | | : | | | | | | | | | |
86 MLCLYHLSNNSVSFFLNPNPDSOGSYFCSLSIFDPPPFQERNLSGGLHIYESQLCCQL 145
| | | | | : | | | | | | | | | | : | | : | | : | | | | | | | | | |
QY 140 K 140
|
Db 146 K 146

Search completed: October 21, 2002, 07:48:51
Job time : 34 secs